*****	(MI)	

protein - protein database search, using Smith-Waterman algorithm

Mon Oct 4 15:24:16 1999; MasPar time 14.68 Seconds 44.916 Million cell updates/sec Run on:

not generated. ular output >MOHAM-312-CLAIM82A.PEP (1-31) from moham312177.pep 227 Title: Description: Perfect Score: Sequence:

87

Claim

XnP

1 hgegtftsdlskqmeeeavrlfiewlknggp 31

PAM 150 Gap 11 Scoring table:

170751 segs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 77:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part33 39:part39

Mean 24.388; Variance 104.481; scale 0.233 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	3.13e-12	3.13e-12	3.13e-12	3.13e-12	3.13e-12	1.39e-11	1.39e-11	1.39e-11	1.72e-11	1.72e-11	7.58e-11	2.18e-10	3.33e-10	3.33e-10	3.33e-10	5.08e-10
	Description	Heloderma suspectum e	Exendin-4, for use in	Gila monster exendin-	Heloderma suspectum e	Heloderma suspectum p	Exendin-3, for use in	Heloderma horridum ex	Gila monster exendin-	Exendin-4 (1-30) for	Heloderma suspectum e	H. horridum exendin-4	H. horridum exendin-4	Exendin-4 (1-28) amid	H. horridum exendin-3	H. horridum exendin-3	H. horridum exendin-4
	ID	R80543	W61770	W47609	R80546	W70288	W61769	R80545	W47608	W61771	R80544	W39302	W39309	W61772	W39368	W39301	W39312
	DB	14	33	30	14	35	39	74	30	39	14	53	53	33	53	53	53
	Length	31	39	39	33	87	39	39	39	30	31	30	30	28	30	30	. 30
Onerv	Match	100.0	100.0	100.0	100.0	100.0	6.96	6.96	6.96	96.5	96.5	93.4	91.2	90.3	80.3	90.3	89.4
	Score	227	227	227	227	227	220	220	220	219	219	212	207	202	205	202	203
Result	NO.		7	e	4	Ŋ	9	7		o	10	11	12	13	14	15	16
	C	Ouery Score Match Length DB ID Description Pred.	Ouery Score Match Length DB ID Description Pred. 227 100.0 3114 R80343 Heloderma suspectum e 3.13e-	Ouery Score Match Length DB ID Description Pred. 227 100.0 31 14 R80543 Heloderma suspectum e 3.13e- 227 100.0 39 39 W61770 Exendin-4, for use in 3.13e-	Ouery Score Match Length DB ID Description Pred. 227 100.0 31 14 R80543 Heloderma suspectum e 3.13e- 227 100.0 39 39 W61770 Exendin-4, for use in 3.13e- 227 100.0 39 30 W47609 Gila monster exendin-3.13e-	Score Match Length DB ID Description Pred. 227 100.0 314 R80543 Heloderma suspectum e 3.13e- 227 100.0 39 39 W61770 Exendin-4, for use in 3.13e- 227 100.0 39 31 R80546 Heloderma suspectum e 3.13e- 227 100.0 39 4 R80546 Heloderma suspectum e 3.13e-	Ouery Score Match Length DB ID Description Pred. 227 100.0 31 14 R80543 Heloderma suspectum e 3.13e- 227 100.0 39 39 W61770 Exendin-4, for use in 3.13e- 227 100.0 39 34 W47609 Glla monster exendin-3.13e- 227 100.0 39 14 R80546 Heloderma suspectum e 3.13e- 227 100.0 87 35 W70288 Heloderma suspectum p 3.13e-	Ouery Score Match Length DB ID Description Pred. 227 100.0 31 14 R80543 Heloderma suspectum e 3.13e- 227 100.0 39 39 W61770 Exendin-4, for use in 3.13e- 227 100.0 39 30 W47609 Gila monster exendin-3.13e- 227 100.0 39 14 R80546 Heloderma suspectum e 3.13e- 227 100.0 87 35 W70288 Heloderma suspectum p 3.13e- 227 100.0 97 39 W61769 Exendin-3, for use in 1.39e-	Ouery Score Match Length DB ID Description 227 100.0 39 39 W61770 Exendin-4, for use in 3.13e- 227 100.0 39 34 W7509 Gilla monster exendin- 227 100.0 39 34 R80546 Heloderma suspectum p 3.13e- 227 100.0 87 35 W70288 Heloderma suspectum p 3.13e- 220 96.9 39 39 4 W80545 Heloderma horizidum ex in 139e- 220 96.9 39 14 R80545 Heloderma horizidum ex in 139e-	Ouery Score Match Length DB ID Description 227 100.0 39 39 W61770 Exendin-4, for use in 3.13e- 227 100.0 39 39 W61770 Glla monster exendin- 227 100.0 39 14 R80548 Heloderma suspectum e 3.13e- 227 100.0 39 14 R80548 Heloderma suspectum e 3.13e- 227 100.0 87 35 W70288 Heloderma suspectum p 3.13e- 220 96.9 39 39 W61769 Exendin-3, for use in 1.39e- 220 96.9 39 30 W47608 Glla monster exendin- 1.39e-	Ouery Score Match Length DB ID Description Pred. 227 100.0 31 14 R80543 Heloderma suspectum e 3.13e- 227 100.0 39 39 W61770 Exendin-4, for use in 3.13e- 227 100.0 39 14 R80546 Heloderma suspectum e 3.13e- 227 100.0 39 14 R80546 Heloderma suspectum p 3.13e- 220 96.9 39 39 W61769 Exendin-3, for use in 1.39e- 220 96.9 39 30 W47609 Gila monster exendin- 220 96.9 39 30 W47609 Gila monster exendin- 220 96.9 39 30 W47609 Gila monster exendin- 220 96.9 39 W61711 Exendin-4 (1.30) for 1.72e-	Ouery Score Match Length DB ID Description Pred. 27 100.0 314 R80543 Heloderma suspectum e 3.13e- 27 100.0 39 39 W61770 Exendin-4, for use in 3.13e- 27 100.0 39 34 R80546 Heloderma suspectum e 3.13e- 27 100.0 87 35 W70288 Heloderma suspectum p 3.13e- 220 96.9 39 39 W61769 Exendin-3, for use in 1.39e- 220 96.9 39 30 W47608 Gila monster exendin- 220 96.9 39 30 W47608 Gila monster exendin- 220 96.9 39 30 W47608 Gila monster exendin- 2219 96.5 30 39 W61771 Exendin-4, for use in 1.39e- 222 96.9 39 30 W47608 Gila monster exendin- 223 96.5 30 39 W61771 Exendin-4 (1.30) for 1.72e- 224 96.5 31 34 R80544 Heloderma suspectum e 1.72e-	Ouery Score Match Length DB ID Description 227 100.0 39 39 W61770 Exendin-4, for use in 3.13e- 227 100.0 39 39 W61770 Glla monster exendin- 227 100.0 39 39 W61770 Glla monster exendin- 227 100.0 39 39 W61769 Heloderma suspectum p 3.13e- 220 100.0 87 35 W70288 Heloderma suspectum p 3.13e- 220 96.9 39 39 W61769 Exendin-3 for use in 1.39e- 220 96.9 39 14 R80545 Heloderma horridum ex 1.39e- 220 96.9 39 30 W47608 Glla monster exendin- 220 96.9 39 30 W47608 Glla monster exendin- 220 96.9 39 30 W47608 Heloderma suspectum e 1.72e- 2219 96.5 31 14 R80544 Heloderma suspectum e 1.72e- 222 96.9 39 30 W47608 Glla monster exendin- 223 96.5 31 24 R80544 Heloderma suspectum e 1.72e- 224 96.5 31 24 W80544 Heloderma suspectum e 1.72e- 225 96.9 39 W61771 Exendin-4 (1.30) for 1.72e- 226 96.9 39 W61771 Exendin-4 (1.30) for 1.72e- 227 96.5 31 24 W80544 Heloderma suspectum e 1.72e- 228 96.5 31 24 W80544 Heloderma suspectum e 1.72e-	Ouery Score Match Length DB ID Description 227 100.0 39 39 W61770 Exendin-4, for use in 3.13e-227 100.0 39 14 R80543 Heloderma suspectum e 3.13e-227 100.0 39 14 R80546 Heloderma suspectum e 3.13e-227 100.0 39 14 R80546 Heloderma suspectum e 3.13e-227 100.0 87 39 W61769 Exendin-3, for use in 1.39e-220 96.9 39 39 W61769 Exendin-3, for use in 1.39e-220 96.9 39 30 W47609 Gila monster exendin-1.39e-220 96.5 31 14 R80544 Heloderma horridum ex 1.72e-219 96.5 31 14 R80544 Heloderma suspectum e 1.72e-219 30.3 W61771 Exendin-4 (1-30) for 1.72e-219 30.3 W61771 Exendin-4 (1-30) for 1.72e-212 93.4 30 29 W39309 H. horridum exendin-4 2.18e-212 93.4 30.29 W39309 H. horridum exendin-4 2.18e-218	Ouery Score Match Length DB ID Description 227 100.0 39 39 W61770 Exendin-4, for use in 3.13e-27 100.0 39 39 W61770 Exendin-4, for use in 3.13e-27 100.0 39 39 W61770 Exendin-4, for use in 3.13e-27 100.0 39 39 W61770 Exendin-7, for use in 3.13e-27 100.0 87 35 W70288 Heloderma suspectum p 3.13e-220 96.9 39 34 R80545 Heloderma suspectum p 3.13e-220 96.9 39 30 W47608 Exendin-7, for use in 1.39e-220 96.9 39 30 W47608 Gila monster exendin-1.39e-219 96.5 30 39 W47708 Exendin-4 (1.30) for 1.72e-219 96.5 30 39 W47708 Heloderma suspectum exendin-1.72e-219 96.5 30 39 W47703 Exendin-4 (1.30) for 1.72e-219 96.5 30 39 W47772 Exendin-4 (1.23) and 3.33e-20 90.3 39 W61772 Exendin-4 (1.28) amid 3.33e-20 90.3 38 W61772 Exendin-4 (1.28) amid 3.33e-20 90.3 39 W61772 Exendin-4 (1.28) amid 3.33e-20 90.3 30 W61772 Exendin-4 (1.28) amid 3.33e-20 90.3 40.30 40.30 40.30 40.30 40.30 40.30 40.30 40.30 40.30 40.30 40.30 40.30 40.30 40.30 40.30 40.30 40.30 4	Ouery Score Match Length DB ID 227 100.0 39 39 W61770 Exendin-4, for use in 3.13e-227 100.0 39 39 W61770 Glia monster exendin-13.13e-227 100.0 39 39 W61770 Glia monster exendin-13.13e-227 100.0 39 39 W61769 Glia monster exendin-13.13e-220 96.9 39 39 W61769 Exendin-3 for use in 1.39e-220 96.9 39 30 W47609 Glia monster exendin-13.13e-220 96.9 39 30 W47608 Glia monster exendin-13.13e-220 96.9 39 30 W47608 Glia monster exendin-17.2e-220 96.9 30 39 W39302 H. horridum exendin-4 2.18e-220 96.9 39 W39308 H. horridum exendin-4 2.18e-220 90.3 30 W39309 H. horridum exendin-4 2.18e-220 90.3 30 W39308 H. horridum exendin-3 3.33e-220 90.3 W39308 H. horridum exendin-3 3.33e-220 90.3 90.3 90.3 W39308 H. horridum exendin-3 3.33e-220 90.3 90.3 90.3 90.3 90.3 90.3 90.3 90.	Ouery Score Match Length DB ID Description 227 100.0 31 14 R80543 Heloderma suspectum e 3.13e- 227 100.0 39 39 W61770 Exendin-4, for use in 3.13e- 227 100.0 39 14 R80546 Heloderma suspectum e 3.13e- 227 100.0 39 14 R80546 Heloderma suspectum e 3.13e- 220 96.9 39 39 W61769 Exendin-3, for use in 1.39e- 220 96.9 39 39 W61769 Exendin-3, for use in 1.39e- 220 96.9 39 30 W47669 Gila monster exendin- 220 96.9 39 30 W47669 Exendin-4 (1-30) for 1.72e- 219 96.5 31 14 R8054 Heloderma suspectum e 1.72e- 219 96.5 31 14 R8054 Heloderma suspectum e 1.72e- 219 96.5 31 14 R8054 Heloderma suspectum e 1.72e- 220 96.9 W61771 Exendin-4 (1-30) for 1.72e- 220 96.9 W61771 Exendin-4 (1-30) for 1.72e- 220 96.9 W61771 Exendin-4 (1-30) for 1.72e- 220 96.3 30 39 W39309 H. horridum exendin-4 2.18e- 225 90.3 30 29 W39301 H. horridum exendin-3 3.33e- 225 90.3 30 29 W39301 H. horridum exendin-3 3.33e- 225 90.3 30 29 W39301 H. horridum exendin-3 3.33e-

27e-1 74e-1 74e-1 74e-1	.55e-1 .18e-0 .18e-0 .18e-0 .45e-0	.80e-0 .80e-0 .80e-0 .21e-0	376	.37e-0 .37e-0 .37e-0 .37e-0 .16e-0
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71 118 20 20	2 2 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	22 28 30 31 31) W.	244444 20110848

ALIGNMENTS

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Eng 7;
WPIL 92-262627/34.
Stimulating/inhibiting insulin release with exendin polypeptide(s) -
Stimulating/inhibiting insulin release with exendin polypeptide(s) -
for treating diabetes mellitus and preventing hyperglycaemia.
Graim 1: Columns 13-14: 17pp: English.
R80543 is the Heloderma suspectum exendin 4 residues 1-31. It is an
insulinotropic peptide, and can therefore be used in the treatment of
diabetes mellitus (types I or II), and for the prevention of
hyperglycaemia. It normalises hyperglycaemia through glucose-dependent
and insulin (in)dependent mechanisms.
Sequence 31 AA;
                                                                                                         R80543;
27-FEB-1996 (first entry)
Heloderma suspectum exendin-4 residues 1-31 (Exendin-4(1-31)).
Exendin-4; residues 1-31; Exendin-4(1-31); diabetes mellitus;
hyperglycaemia; insulinotropic peptide.
                                                       R80543 standard; peptide; 31 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUN-1995.
24-MAY-1993; 066480.
24-MAY-1993; US-066480.
(ENGJ/) ENG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5424286-A.
RESULTANT MADE TO THE STATE OF THE STATE OF
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Score 227; DB 14; Length 31; Pred. No. 3.13e-12; 0; Mismatches 0; Indels Query Match 100.0%; Best Local Similarity 100.0%; Matches 31; Conservative

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Gaps

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RESULT ID W6 AC W6 DT 29 DE EX

LT 2
W61770 standard; peptide; 39 AA.
W61770 standard; peptide; 39 AA.
W61770 standard; peptide; 39 AA.
S9-WAR-1999 (first entry)
Exendin-4, for use in treating disorders related to food intake.
Exendin-4, for use II diabetes; eating disorders; cardiac disease;

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Query Match
                      imaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R80546;
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MARIL.) AMILIN PHRAKM INC.

Beeley NRA, Bhavsar S, Prickett KS;

RPI: 98-398796/34.

The Pile od intake by administering exendins or their analogues - for treatment of e.g. obesity, type II diabetes, eating disorders and insulin resistance

Claims 17, 25; Page 8; 214pp; English.

The invention relates to a new method for treating disorders that are alleviated by reducing food intake, in particular obesity, type II diabetes, eating disorders, insulin resistance syndrome, elevated plasma glucose levels, or the risk of cardiac disease. The method comprises administering an exendin or an exendin agonist. The treatment reduces appetite and lowers plasma lipid levels. It inhibits food consumption as effectively as amylin or cholecystokinin but has a much longer-lasting action (still effective after 6 hours in a mouse model).

The present sequence is that of exendin-4 which is one of the preferred companies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Regulating gastrointestinal motility using exendins or their agonists for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations Claims 20 and 21; Fig 1; 70pp; English.
W47549 describes a generic exendin agonist, provided that it does have the formula of either exendin-3 (W47608) or exendin-4
syndrome; elevated plasma glucose level; agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                emptying, can be, used to treat spasm (where associated with acute diverticulities or disorders of the biliary tract or sphincter of odd), postprandial dumpling syndrome and hyperslycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stromach contents passing into the administered to subjects undergoing gastrointestinal diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exendin agonist; gastric motility; gastric emptying; treatment; spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type 1 diabetes; impaired glucose tolerance; toxin ingestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exendin agonists, which reduce gastric motility and delay gastric
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08-AUG-1997; U14199.
08-AUG-1995; US-694954.
(AMTL-) AMTLIN PHARM INC.
Beeley NRA, Gedulin B, Prickett KS, Young AA;
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Best Local Similarity 100.0%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W47609 standard, peptide, 3
W47609;
03-JUL-1998 (first entry)
                                                                  16-JUL-1998.
07-DAN-1998; U00449.
14-NOV-1997; US-066029.
07-JAN-1997; US-055404.
14-NOV-1997; US-055404.
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insulin resistance
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06-NOV-1998 (first entry)
Heloderma suspectum proexendin peptide.
Heloderma suspectum proexendin; exendin N-terminal peptide; ENTP;
Heloderma suspectum proexendin; gene; Heloderma horridum; metabolic disease;
drug screening; endocrine tumour; organ failure; cell metabolism;
diabetes; reptilian venom peptide.
                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insulinotropic peptide, and can therefore be used in the treatment of diabetes mellitus (types I or II), and for the prevention of hyperglycaemia. It normalises hyperglycaemia through glucose-dependent and insulin-in) dependent mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-1996 (first entry)
Heloderma suspectum exendin-4.
Exendin-4; diabetes mellitus; hyperglycaemia; insulinotropic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stimulating/inhibiting insulin release with exendin polypeptide(s) for treating diabetes mellitus and preventing hyperglycaemia. Claim 6; Columns 13-14; 17pp; English. R80346 is Heloderma suspectum exendin-4. It is an
                                          Exendins, components of Glia monster venum, many components similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.

Sequence 39 AA;
investigation, particularly radiological or by magnetic resonance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 227; DB 14; Length 39; Pred. No. 3.13e-12;
                                                                                                                                                                                  Length 39
                                                                                                                                                                                                                             Indels
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Pred. No. 3.13e-12;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                             1 hgegtftsdlskqmeeeavrlfiewlknggp 31
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/note= "Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W70288 standard; Protein; 87 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              R80546 standard; peptide; 39 AA.
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                                                                                                                                                                       Local Similarity 100.0%; (es 31; Conservation)
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24-MAY-1993; 066480.
24-MAY-1993; US-066480.
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/note-
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/note=
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/note=
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04-FEB-1998; CA0071.
07-FEB-1997; GB-002582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heloderma suspectum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ENGJ/) ENG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cleavage_site
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Fig. 1935, 933103.

The includent acid encoding proexendin - used to diagnose and treat, e.g. endocrine tumours, also to treat poisoning by reptile venom as includent acid encoded by its constant as isolated from a H. suspectum salivary gland cDNA library.

The Proexendin protein comprises of a novel exendin N-terminal peptide (ENTP) linked to the N-terminus of the exendin A peptide by a consensus dipeptidyl peptidase cleavage site. The proexendin conn is gene of Heloderma horidum, mutant alleles and proexendin gene of Heloderma horidum, mutant alleles and proexendin gene of Heloderma horidum, mutant alleles and proexendin gene regulatory defects associated with metabolic disease) and species homologues (e.g. for developing animal models for drug screening). The proexendin peptide can be used to raise antibodies. Anti-proexendin antibodies are claimed to be useful for diagnosing conditions associated with altered levels of proexendin (e.g. endocrine tumours and organ failure), for identifying other regulators of cell metabolism, in drug screens and for treating metabolic diseases (e.g. diabetes) and for neutralising, or detecting, reptilian venom peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reducing food intake by administering exendins or their analogues - for treatment of e.g. obesity, type II diabetes, eating disorders and insulin resistance claims 16, 24; Page 8; 214pp; English.

Claims 16, 24; Page 8; 214pp; English.

The invention relates to a new method for treating disorders that are are alleviated by reducing food intake, in particular obesity, type II diabetes, eating disorders, insulin resistance syndrome, elevated plasma glucose levels, or the risk of cardiac disease. The method comprises administering an exendin or an exendin agonist. The treatment reduces appetite and lowers plasma lipid levels. It inhibits food consumption as effectively as amylin or cholecystokinin but has a much longer lasting action (still effective after 6 hours in a mouse model).

The present sequence is that of exendin-3 which is one of the preferred compounds for use in the method.
Sequence 39 AA;
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Exendin-3, for use in treating disorders related to food intake.
Exendin; obesity; type II diabetes; eating disorders; cardiac disease; insulin resistance syndrome; elevated plasma glucose level; agonist.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 87;
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Pred. No. 3.13e-12;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beeley NRA, Bhavsar S, Prickett KS; WPI; 98-398796/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W61769 standard; peptide; 39 AA.
W61769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%;
Local Similarity 100.0%;
nes 31; Conservative
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14-NOV-1997; US-066029.
07-JAN-1997; US-034905.
08-AUG-1997; US-055404.
14-NOV-1997; US-065442.
(AMXL-) AMXLIN PHARM INC.
05-FEB-1997; US-037412.
(ONEO-) 1149336 ONTARIO
Drucker DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heloderma horridum
WO9830231-A1.
                                                                WPI; 98-447230/38.
N-PSDB; V33163.
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WEST 95-262627/34.

Stimulating finititing insulin release with exendin polypeptide(s) Stimulating finititing insulin release with exendin polypeptide(s) for treating diabetes mellitus and preventing hyperglycaemia.

Claim 5: Columns 13-14; 17pp; English.

R80545 is Heloderma horridum exendin-3. It is an
insulinotropic peptide, and can therefore be used in the treatment of
diabetes mellitus (types I or II), and for the prevention of
hyperglycaemia. It normalises hyperglycaemia through glucose-dependent
and insulin-(in)dependent mechanisms.

Score 220; DB 14; Length 39;

Heloderma horridum exendin-3.
Exendin-3; diabetes mellitus; hyperglycaemia; insulinotropic peptide.
Reloderma horridum.

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LT 7 R80545 standard; peptide; 39 R80545;

27-FEB-1996 (first entry)

24-MAY-1993; 066480. 24-MAY-1993; US-066480. (ENGJ/) ENG J.

Eng J;

13-JUN-1995

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Regulating gastrointestinal motility using exendins or their agonists - for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations claims 20 and 21; Fig 1; 70pp; English.

W47549 describes a generic exendin agonist, provided that it does have the formula of either exendin-3 (W47608) or exendin-4
                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gila monster exendin-3.

Exendin agonist; gastric motility; gastric emptying; treatment; spasm; postprandial dumping syndrome; postprandial hyperglycaemia; spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type I diabetes; impaired glucose tolerance; toxin ingestion; obesity; Gila monster venom; exendin-3.

Reloderma horridum.
                                                                                    ö
        Score 220,
Pred. No. 1.39e-11;
...ma+ches 0; Indels
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08-AUG-1997; UJ4199.
08-AUG-1996; US-694954.
6AMIL-) AMYLIN PHARM INC.
6ABLEY NRA, Gedulin B, Prickett KS, Young AA; WPI; 98-145351/13.
                                                                                                                                                                                                                     hsdgtftsdlskqmeeeavrlfiewlknggp 31
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W47608 standard; peptide; 39
W47608;
Query Match
Best Local Similarity 93.5%;
Matches 29; Conservative
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Modified_site
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1 hsdgtftsdlskqmeeeavrlfiewlknggp 31

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The invention relates to a new method for treating disorders that are alleviated by reducing food intake, in particular obesity, type II diabetes, eating disorders, insulin resistance syndrome, elevated plasma glucose levels, or the risk of cardiac disease. The method comprises administering an exendin or an exendin agonist. The treatment reduces appetite and lowers plasma lipid levels. It inhibits food consumption as effectively as amylin or cholecystokinin but has a much longer-lasting action (still effective after 6 hours in a mouse model). The present sequence is that of exendin-4 (1-30) or its amide which is sequence 30 AA;
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                                                                                                                                                                                                                                                                                                                                              29-WAR-1999 (first entry)
Exendin-4 (1-30) for use in treating disorders related to food intake.
Exendin; obesity: type II diabetes; eating disorders; cardiac disease; insulin resistance syndrome; elevated plasma glucose level; agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                Gaps
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Heloderma suspectum exendin-4 residues 1-31-Tyr31.
Exendin-4; residues 1-31; Y-31-Exendin-4(1-31); diabetes mellitus; hyperglycaemia; Tyr31; insulinotropic peptide.
                                                 similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia. Sequence 39 AR:
   investigation, particularly radiological or by magnetic resonance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beeley NRA, Bhavar S, Prickett KS;
NPI: 98-398796/34.
Reducing food intake by administering exendins or their
analogues - for treatment of e.g. obesity, type II diabetes,
eating disorders and insulin resistance
                                                                                                                                         Score 220; DB 30; Length 39;
Pred. No. 1.39e-11;
2; Mismatches 0; Indels
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Pred. No. 1.72e-11;
0; Mismatches 0; Indels
                                        have some
                                 Exendins, components of Gila monster venom,
                                                                                                                                                                                                          1 hsdgtftsdlskgmeeeavrlfiewlknggp 31
                                                                                                                                                                                                                              | hgegtftsdlskqmeeeavrlfiewlknggp 31
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R80544 standard; peptide; 31 AA.
                                                                                                                                                                                                                                                                                             .ULT 9 W61771 standard; peptide; 30 AA. W61771;
                                                                                                                                        96.9%;
larity 93.5%; Conservative
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Best Local Similarity 100.0%;
Matches 30; Conservative
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16-JUL-1998,
07-JAN-1998; U00449,
07-1997; US-066029,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-NOV-1997; US-066029.
07-JAN-1997; US-034905.
08-AUG-1997; US-055404.
14-NOV-1997; US-055442.
                                                                                                                                                                                                                                                                                                                                                                                                                      Heloderma suspectum.
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US5424286-A.
13-JUN-1995.
                                                                                                                                                        Local Similarity
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Modified_site
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                  imaging
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W09746584-A1.

W09746584-A1.

PD 11-DEC-1997.

DG 11-DEC-1997.

WE 13-SEP-1996; DE-022502.

R 13-SEP-1996; DE-022502.

R 15-SEP-1996; DE-022502.

R 16-SEP-1996; DE-022502.

R 16-SEP-1996; DE-022502.

R 17 INDICACTE OF ALMANHEIM GMBH.

GOEKE B, GOEKE R, HOffmann E,

WPI; 98-042119/04.

PT TUNDCACTE OF VERSIONS OF Exendin peptide(s) for treating diabetes -

Increase secretion and blosynthesis of insulin, but reduce those of

glucagon, and do not induce hypoglycaemia

PT Increase secretion and blosynthesis of insulin, but reduce those of

glucagon, and do not induce hypoglycaemia to reduce those of

rich speptide is a fragment of exendin-4 isolated from Heloderma

horridum. This peptide and its aalts, esters and derivatives can be

conserted that activity can increase peripheral glucagon, and

independent of this activity can increase peripheral glucagon, and

independent of this activity can increase peripheral glucagon, and

independent of this activity can increase peripheral glucagon.

Exendin-3 and exendin-4 are only active when blood sugar levels are

Exendin-3 and exendin-4 are only active when blood sugar levels are

Exendin-3 and exendin-4 are only active when blood sugar levels are

Exendin-3 and the known exendins, they are more active (effective peptide I (Gib!) and the known exendins, they are more active (effective contractive (effective contractive (effective contractive contractive (effective contractive contr
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                                                                                             WELL 95-262627/34.

Stimulating/inhibiting insulin release with exendin polypeptide(s) -
for treating diabetes mellitus and preventing hyperglycaemia.

Claim 2; Columns 13-14; 17pp; English.

R80544 is the Heloderma suspectum exendin 4 residues 1-31, where
the native pro31 has been replaced with a Tyr residue. It is an
insulinotropic peptide, and can therefore be used in the treatment of
diabetes mellitus (types I or II), and for the prevention of
hyperglycaemia. It normalises hyperglycaemia through glucose-dependent
and insulin_(in)dependent mechanisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-1998 (first entry)
H. horridum exendin-4 peptide.
Exendin-3; exendin 4; dlabetes; insulin; secretion; biosynthesis; glucagon reduction; hypoglycaemia; glucose; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "This residue can be any amino acid except Gly"
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Pred. No. 7.58e-11;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 219; DB 14; Length 31 Pred. No. 1.72e-11; 0; Mismatches 0; Indels
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W39302 standard; peptide; 30 AA.
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Best Local Similarity 100.0%;
Matches 30; Conservative
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Best Local Similarity 100.0%;
Matches 29; Conservative
24-MAY-1993; 066480.
24-MAY-1993; US-066480.
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                                                                                                                                                                                                                                                                                                                                                              31 AA;
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                                                    (ENGJ/) ENG J.
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셤
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LT 12 W39309 standard; peptide; 30 AA.

RESULT ID W3

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Heloderma horridum
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Best Local
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ID W3
AC W3
AC W3
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                                                                                                                                                                                                                                                    Truncated versions of exendin peptide(s) for treating diabetes -
increase secretion and biosynthesis of insulin, but reduce those of
increase secretion and biosynthesis of insulin, but reduce those of
alwagon, and do not induce hypoglycaemia
Claim 2: Page 22: 150pp; English.

Peptides w39303-W39420 are fragments of exendin-3 and exendin-4
isolated from Heloderma horridum which are used in a novel method
for the treatment of diabetes mellitus. These peptides can simulate
biosynthesis and secretion of insulin, but have the opposite effect on
glucagon, and independent of this activity can increase peripheral
culcagon, and independent of this activity can increase peripheral
culcagon, and independent of this activity can increase peripheral
culcagon are high, so they will not induce hypoglycaemia. Compared
with glucagon-like peptide 1 (GLPI) and the known exendins, they are more
active (effective at lower doses), more stable to degradation and
metabolism and have a longer lasting effect. Truncated forms of this
peptide can be made more economically than full length versions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reducing food intake by administering exendins or their analogues - for treatment of e.g. obesity, type II diabetes, eating disorders and insulin resistance (laims 18, 26; Page 12; 21/4pp; English.

The invention relates to a new method for treating disorders that are alleviated by reducing food intake, in particular obesity, type II diabetes, eating disorders, insulin resistance syndrome, elevated plasma glucose levels, or the risk of cardiac disease. The method comprises administering an exendin or an exendin agonist. The treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-1999 (first entry)
Exendin-4 (1-28) amide for use in treating disorders related to food.
Exendin; obesity; type II diabetes; eating disorders; cardiac disease; insulin resistance syndrome; elevated plasma glucose level; agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                           H. horridum exendin-4 peptide derivative #6.
Exendin-3; exendin 4; diabetes; insulin; secretion; biosynthesis;
glucagon reduction; hypoglycaemia; glucose; treatment.
Heloderma horridum.
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                                                                                                                      /note= "C-terminal amide"
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                                                                                       Location/Qualifiers
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WPI; 98-398796/34.
                                                                                                                                                                                                            (BOEF ) BOEHRINGER MANNHEIM GMBH. Goeke B, Goeke R, Hoffmann E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W61772 standard; peptide; 28 AA.
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96.6%;
              (first entry)
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13-SEP-1996; DE-037230.
05-JUN-1996; DE-022502.
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07-JAN-1997; US-034905.
08-AUG-1997; US-055404.
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07-JAN-1998; U00449.
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Matches 28; Conserv
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Modified_site
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                                                                                                                                   WO9746584-A1.
              05-JUN-1998
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Truncated versions of exendin peptide(s) for treating diabetes -
Increase secretion and blosynthesis of insulin, but reduce those of
gluadgon, and do not induce hypoglycaemia
claim 2: Page 27: 150pp; English.

Peptides w39303-W39420 are fragments of exendin-3 and exendin-4
isolated from Heloderma horridum which are used in a novel method
for the treatment of diabetes mellitus. These peptides can stimulate
blosynthesis and secretion of insulin, but have the opposite effect on
glucagon, and independent of this activity can increase peripheral
glucagon, and independent of this activity can increase peripheral
glucagon. Exendin-3 and exendin-4 are only active when blood
sugar levels are high, so they will not induce hypoglycaemia. Compared
with glucagon-like peptide (Girl) and the known exendins, they are more
active (effective at lower doses), more stable to degradation and
metabolism and have a longer lasting effect. Truncated forms of this
peptide can be made more economically than full length versions.
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reduces appetite and lowers plasma lipid levels. It inhibits food consumption as effectively as amylin or cholecystokinin but has a much longer-lasting action (still effective after 6 hours in a mouse model). The present sequence is that of exendin-4 (1-28) amide which is one of the preferred compounds for use in the method.
Sequence 28 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. horridum exendin-3 peptide derivative #11.
Exendin-3; exendin 4; diabetes; insulin; secretion; biosynthesis; glucagon reduction; hypoglycaemia; glucose; treatment.
Heloderma horridum.
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t. boridam exendin-3 peptide.
Exendin-3; exendin 4; diabetes; insulin; secretion; biosynthesis; glucagon reduction; hypoglycaemia; glucose; treatment.
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Pred. No. 3.33e-10;
0; Mismatches 0;
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Goeke B, Goeke R, Hoffmann E;
WPI; 98-042119/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JT 14
W39368 standard; peptide; 30 AA.
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W39301 standard; peptide; 30 AA.
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Best Local Similarity 93.1%;
Matches 27; Conservative
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Local Similarity 100.0%;
nes 28; Conservative
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05-JUN-1998 (first entry)
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05-JUN-1997; E02930.
13-SEP-1996; DE-037230.
05-JUN-1996; DE-022502.
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PARTICLE AND PROBLEM GREATER AND PRICED FOR A COOKER B. GOCKE B. G
                                                                                        05-JUN-1997; E02930.
13-SEP-1996; DE-037230.
05-JUN-1996; DE-022502.
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Ouery Match

Query Match

90.3%; Score 205; DB 29; Length 30;
Best Local Similarity 93.1%; Pred. No. 3.33e-10;
Matches 27; Conservative 2; Mismatches 0; Indels

Gaps ö

Search completed: Mon Oct 4 15:24:34 1999 Job time: 18 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Oct 4 15:23:50 1999; MasPar time 6.03 Seconds 206.071 Million cell updates/sec Run on:

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>MOHAW-312-CLAIM82A.PBP (1-31) from moham312177.pep 227 1 hgegtftsdlskqmeeeavrlfiewlknggp 31

Lacte: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

122810 segs, 40068593 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 34.029; Variance 63.644; scale 0.535 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					SUMMARIES		
		dф					
Result No.	Score	Query Match	Query Match Length DB	DB	a	Description	Pred. No.
1 1	227	100.0	39	: ⊣	HWGH4G	exendin-4 - Gila mons	3.06e-27
7	220	6.96	39	٦	HWGH3Z	١	7.58e-26
m	127	55.9	31	~	S44472	glucagon G2 - North A	2.68e-08
4	127	55.9	101	Н	GCFGB	glucagon precursor -	2.68e-08
2	125	55.1	63	Н	GCIDC		5.97e-08
φ	122	53.7	30	7	S44473	glucagon-like peptide	1.97e-07
7	122	53.7	31	7	S44471	glucagon Gl - North A	1.97e-07
α	121	53.3	30	7	B61125	glucagon-like peptide	2.93e-07
σħ	121	53.3	30	7	C61125	-like	2.93e-07
10	120	52.9	99	N	151093	glucagon - chinook sa	4
11	120	52.9	178	7	151057	glucagon II precursor	4.35e-07
12	120	52.9	178	7	I51058	Н	4.35e-07
13	119	52.4	72	-	GCGXA	14	6.45e-07
14	118	52.0	122	Н	GCAF2	glucagon 2 precursor	9.55e-07
15	117	51.5	9	Н	GCONC	pr	1.41e-06
16	115	50.7	29	Н	GCDF	glucagon - smaller sp	m
17	115	50.7	158		GCPG	precursor	3.08e-06
18	115	50.7	180	N	A57294	glucagon precursor -	3.08e-06
19	115	50.7	180		GCHY	glucagon precursor -	3.08e-06
20	115	50.7	180	Н	GCRIDU	glucagon precursor -	3.08e-06
21	115	50.7	180	Н	GCBO	glucagon precursor -	3.08e-06
22	115	50.7	180	Н	GCGP	glucagon precursor -	3.08e-06
23	115	50.7	180	-	GCHU	glucagon precursor -	3.08e-06

24 115 50.7 180 1 25 114 50.2 206 2 26 114 50.2 206 2 27 113 49.8 124 1 28 108 47.6 29 2 31 104 45.8 29 1 33 100 44.1 29 2 34 40 41.1 29 2 35 100 44.1 29 2 40 96 42.3 29 1 41 96 42.3 29 1 42 99 43.6 29 1 44 99 41.9 29 1 44 19 96 42.3 29 2 44 19 96 42.3 29 2 44 19 96 42.3 29 2 44 19 96 42.3 29 2 44 19 96 42.3 29 2 44 19 96 42.3 29 2 44 19 96 42.3 29 2 44 19 96 42.3 29 1 44 99 43.6 Expend AACRESIONS #modified Experime SUMARY #length 39 #modified Cols. CLASSIFICATION #superfamily gl experime SUMARY #length 39 #modified Ourry Match #formal_name He Doury Match #formal_name He Infilitili	1 GCRT glucagon precursor - 3.08e-06 6 2 I51301 glucagon precursor - 4.54e-06 6 1 GCAF glucagon - chicken 4.54e-06 6 2 I51301 glucagon - chicken 4.54e-06 8 1 GCAF glucagon - Chinchilla 2.11e-05 9 2 S07211 glucagon - marbled el 4.52e-05 9 1 GCRLE glucagon - Diopean f 2.04e-04 7 1 GCRIS glucagon - Diopean f 2.04e-04 9 2 A91742 glucagon - Arabian ca 8.56e-04 9 2 A91742 glucagon - Arabian ca 8.56e-04 9 2 GCRGG glucagon - common squ 8.56e-04 9 2 GCRGG glucagon - common squ 8.56e-04 9 1 GCLGG glucagon - common squ 8.56e-04 9 2 GCRGG glucagon - common squ 8.56e-04 9 1 GCCRG glucagon - clephantfi 1.29e-03 9 1 GCCR glucagon - elephantfi 1.29e-03 9 1 GCCR glucagon - clephantfi 1.29e-03 9 1 GCTR glucagon - ostrich 5.50e-03 9 1 GCTR glucagon - ostrich 5.50e-03 9 1 GCTR glucagon - duck 5.50e-03	ALIGNMENTS	<pre>#type complete - Gila monster ame Heloderma suspectum #common_name Gila monster 93 #sequence_revision 31-Mar-1993 #text_change 1907</pre>	Kleinman, W.A.; Singh, L.; Singh, G.; Raufman, J.P. Chem. (1992) 267:7402-7405 n and characterization of exendin-4, an exendin-3 ne, from Heloderma suspectum venom. Further evidence exendin receptor on dispersed acini from guinea pig	92218391 ein ##!abel ENG not stimulate amylase secretion by pancreatic acinar	ily glucagon carboxyl end; duplication; venom ified_site amidated carboxyl end (Ser) #status	#molecular-weight 418.	Pred. No. 3.06e- 0; Mismatches 0: FIEWLKNGGP 31 fiewlknggp 31	<pre>#type complete _name Heloderma horridum #common_name Mexican beaded d d v-1997 v-1997 hddrews, P.C.; Kleinman, W.A.; Singh, L.; Raufman, hddrews, P.C.; Kleinman, W.A.; Singh, L.; Raufman,</pre>
24 115 25 114 26 113 28 119 29 1108 30 1104 31 1104 31 1104 32 1104 33 1100 34 1100 35 1100 36 40 96 42 99 42 99 43 99 39 99 44 995 44 995 44 995 44 995 44 995 44 995 44 995 44 995 44 995 44 995 44 995 44 995 45 91 WHENT Exen Cession ##residue #	000000		HWGH4G exendin- #formal_1 31-Mar-18	A42486 A42486 Eng, J.; J. Biol. Isolation analogn for an	ences MUID A42486 e_type profis s 1-34	erf late	*length	milarity l .; Conserv. FTSDLSKQME: 	HWGH3Z exendin- *formal_ 1izard 31-mard 21-Nov A23674 A23674 Eng, J.;
		E	ISM	CESSIONS FERENCE #authors #journal #title	ess; #mo]	ce JASSIFICATION SYWORDS SATURE 39	Match	Best Loc Matches	LT E NISM SSIONS RENCE

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J. Biol. Chem. (1988) 263:9746-9751
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Best Local Similarity :
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#title
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FEATURE
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37-67
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                                                                                               ##residues 1-39 ##label ENG
NT Exendins are venom components that are thought to bind to receptors
for vascactive intestinal peptide and/or secretin on pancreatic
acinar cells and activate adenylate cyclase, resulting in
secretion of amylase.
IFICATION #superfamily glucagon
RDS amidated carboxyl end; duplication; secretagogue; venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.
Blochen, J. (1994) 8108:339-345
Characterization of insulins and proglucagon-derived peptides
from a phylogenetically ancient fish, the paddlefish
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the sequence from Fig. 3 is inconsistent with that from
Fig. 5 in having 29-61u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glucagon; glucagon-36 (oxyntomodulin); glucagon-like peptide
1; glucagon-like peptide 2
*formal_name Rana catesbeiana *common_name bullfrog
31-Mar-1993 *sequence_revision 31-Mar-1993 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        944472 #type complete
glucagon G2 - North American paddlefish (Polyodon spathula)
#formal_name Polyodon spathula
19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change
20-Mar-1998
#journal J. Biol. Chem. (1990) 265:20259-20262
#title Purification and structure of exendin-3, a new pancreatic Secretagogue isolated from Heloderma horridum venom.
#cross-references MID:91056067
#accession A23674
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Pollock, H.G.; Hamilton, J.W.; Rouse, J.B.; Ebner, K.E.;
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#length 31 #molecular-weight 3682 #checksum 7826
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                                                                                                                                                                                                                                                         experimental
#length 39 #molecular-weight 4204
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Pred. No. 7.58e-26;
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Pred. No. 2.68e-08;
                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-Mar-1998
B28091; C28091; D28091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Polyodon spathula).
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Local Similarity 93.5%;
Les 29; Conservative
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larity 55.2%;
Conservative
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                                                                              ##molecule_type protein
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es 16; Conser
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##note
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ALTERNATE_NAMES
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33
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glucagon precursor - channel catfish (fragments)
#formal_name Ictalurus punctatus #common_name channel catfish
31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
20-Mar-1998
A05166; A05167
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*product glucagon-like peptide 1 *status experimental
*label GLI\
*product glucagon-like peptide 2 *status experimental
*label GL2
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#product glucagon-like peptide 1 #status experimental
#label GL1
                                                                                                                                                                                                                                          ##molecule_type protein
##residues 30-63 ##label AND2
#FICATION #superfamily glucagon
RDS carbohydrate metabolism; duplication; hormone; pancreas
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Isolation of pertide hormones from the pancreas of the bullfrog (Rana catesbelana). Amino acid sequences of pancreatic polypeptide, oxyntomodulin, and two glucagon-like peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Andrews, P.C.; Ronner, P.
#journal J. Biol. Chem. (1985) 260:3910-3914
#title Isolattion and structures of glucagon and glucagon-like peptide from catfish pancreas.
#cross-references MUID:85157536
                                                                                                                                                                                                                                                                                                                                                            #product glucagon-36 (oxyntomodulin) #status
experimental #label G36\/
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Pred. No. 5.97e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.9%; Score 127; DB 1; Lel
51.6%; Fred. No. 2.68e-08;
Mismatches 7;
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                                                                                                                                                                              ##molecule_type protein
##residues 37-68 ##label POL
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##residues 1-29 ##label AND1
                                                                                                                 ##molecule_type protein
##residues 1-36 ##label PO2
                                                                                toross-references MUID:88257102
taccession B28091
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Matches 15; Conservative
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Mol. Endocrinol. (1995) 9:267-277
Trout and chicken proglucagon: alternative splicing generates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Conlon, J.M.; Andrews, P.C.; Thim, L.; Moon, T.W.
#journal Gen. Comp. Endocrinol. (1991) 82:23-32
#title The primary structure of glucagon-like peptide but not insulin has been conserved between the American eel,
Anguilla rostrata and the European eel, Anguilla anguilla.
#cross-references MIDI:91340068
#accession C61125
#journal Gen. Comp. Endocrinol. (1991) 82:23-32
#title The primary structure of glucagon-like peptide but not insulin has been conserved between the American eel, Anguilla rostrata and the European eel, Anguilla anguilla.#cross-references MUID:91340068
#accession B61125
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#formal_name Oncorhynchus tschawytscha #common_name chinook
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#label GLP\
#modified_site amidated carboxyl end (Arg) #status
predicted
#length 30 #molecular-weight 3376 #checksum 6092
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glucagon-like peptide - European eel
*formal_name Anguilla anguilla *common_name European eel
10-Mar-1994 *sequence_revision 10-Mar-1994 *text_change
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Pred. No. 2.93e-07;
...matches 6; Indels
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Local Similarity 48.3%;
hes 14; Conservative
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Best Local Similarity 48.3%;
Matches 14; Conservative
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Blochen. J. (1994) 300:339-345
Characterization of insulins and proglucagon-derived peptides
from a phylogenetically ancient fish, the paddlefish
                                                                                                                                                                                                                                      Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.
Biochem. J. (1994) 300:339-345
Characterization of insulins and proglucagon-derived peptides
from a phylogenetically ancient fish, the paddlefish
(Polyodon spathula).
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#formal_name Polyodon spathula
18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change
                    B61125 #type complete
glucagon-like peptide - American eel
#formal_name Anguilla rostrata #common_name American eel
10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change
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"AASSIFICATION #superfamily glucagon
"WORDS carbohydrate metabolism; duplication; hormone; pancreas
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20-Mar-1998
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#length 31 #molecular-weight 3751 #checksum 7808
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Conlon, J.M.; Andrews, P.C.; Thim, L.; Moon, T.W.
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Pred. No. 1.97e-07;
"...matches 6; Indels
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Best Local Similarity 55.2%;
Matches 16; Conservative
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Best Local Similarity 55.2%;
Matches 16; Conservative
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Query Match 52,9%;
Best Local Similarity 44,8%;
Matches 13; Conservative
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FERENCE A55895
#authors Irwin, D.M.; Wong, J.
#fournal Mol. Endocrinol. (1995) 9:267-277
#title Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.
#accession I51057
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glucagon I precursor - rainbow trout
#formal_name Oncorhynchus mykiss #common_name rainbow trout
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
21-Nov-1997
IS1058; IS1299; IS1056; IS1037; IS1036; IS1300
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duplication
*length 178 *molecular-weight 19998 *checksum
                                       **status preliminary; translated from GB/EMBL/DDBJ
**molecule_type mRNA
**#resident
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##molecule_type DNA
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##cross-references EMBL:U19914; NID:9736362; PID:9736363
cession 151039
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Pred. No. 4.35e-07;
11; Mismatches 5; Indels
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Pred. No. 4.35e-07;
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Mol. Endocrinol. (1995) 9:267-277
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*length 66 *checksum
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larity 44.8%;
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#title Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.
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glucagon; glucagon-36 (oxyntomodulin); glucagon.like peptide
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NID:q999384; PID:q999385
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#molecule_type mRNA
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##cross-references GB:S78473; NID:g999382; PID:g999383
##cross-references GB:S78473; NID:g999382; PID:g999383
##cross-references GB:S78473; NID:g999382; PID:g999383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-172 | 113-
                                                                                                                    ##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
##rosia...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##Status
##molecule_type DNA
##rooi-cule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues __ 58-123 ##label IR3
##cross-references EMBL:019913; NID:9736360; PID:9736361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #*cross-references EMBL:U19919; NID:9736374; PID:9736377
cession I51036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 120; DB 2; Ler
Pred. No. 4.35e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'M',114-144 ##label IR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 HADGIYISDVSTYLQDQAAKDFVSWLKSG 118
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                                                                                                                                                                                                                                         1-178 ##label IRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123/2
#superfamily glucagon
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##residues 1-36 ##label POL
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*authors Plisetskaya, E.; Pollock, H.G.; Rouse, J.B.; Hamilton, J.W.; Kimmel, J.R.; Gorbman, A. **

#journal Regul Pept. (1986) 14:57-67

#title Regul Pept. (1986) 14:57-67

#title Isolation and structure of coho salmon (Oncorhynchus kisutch) glucagon and glucagon-like peptide.

#cross-references MUID:86234328

#accession JPO13

##molecule_type protein

##residues 1-29;30-60 ##label.PLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #domain signal sequence #status predicted #label SIGN
*product proglucagon 2 #status predicted #label PGC2N
*product glucagon #status predicted #label GCNN
*product glucagon-like peptide 1 #status predicted
#label GLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucagon precursor - coho salmon (fragments)
glucagon; glucagon-like peptide 1
formal_name Oncorhynchus kisutch #common_name coho salmon
30-sep-1988 #sequence_revision 30-Sep-1988 #text_change
20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOESTON
##rolecule_type mRNA
##residues 1-122 ##label LUN
##cross-references GB:J00933; NID:g213352; PID:g213353
IFICATION #superfamily glucagon
RDS carbohydrate metabolism; duplication; hormone; pancreas
Gaps
                                                                                                                                                                                                                                                                                                                                        GCAF2 *type complete
glucagon 2 precursor - American goosefish
glucagon; glucagon-like peptide 1
glucagon; glucagon-like peptide 1
goosefish
31-Mar-1993 *sequence_revision 31-Mar-1993 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Lund, P.K.; Goodman, R.H.; Montminy, M.R.; Dee, P.C.;
Habener, J.F.

#journal J. Biol. Chem. (1983) 258:3280-3284

#title Anglerfish islet pre-proglucagon II. Nucleotide and corresponding amino acid sequence of the cDNA.

#cross-references MUID:83135785

#accession A05150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #length 122 #molecular-weight 14171 #checksum 7194
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larity 44.8%; Pred. No. 9.55e-07;
Conservative 10; Mismatches 6; Indels
                                                                                                                                           Length 72;
                                                                                                                                                                                 6; Indels
                                                                                                                                      Query Match 52.4%; Score 119; DB 1; I Best Local Similarity 44.8%; Pred. No. 6.45e-07; Matches 13; Conservative 10; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #type fragments
                                                                                                                                                                                                                  39 HADGIYISDVSSYLQDQAAKKFVTWLKQG 67
                                                                                                                                                                                                                                              JP0103; JP0104
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Matches 13; Conser
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REFERENCE
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52-80
89-119
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CONTAINS
ORGANISM
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                                     39-70
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1-36
                                                                                                SUMMARY
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CLASSIFICATION #superfamily glucagon
KEYWORDS

REMUCES

1-29
#product glucagon #status experimental #label GCN\
30-60
#product glucagon-like peptide 1 #status experimental
#label GLI

CUMMARY

QUERY MAtch
Best Local Similarity 41.4%; Pred. No. 1.41e-06;
Matches 12; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Db 30 HADGTYTSNVSTYLODQAAKDFVSWLKSG 58
|::||:||:||:||:||:||:||:||:||:||:||
Qy 1 hgeqfftsdlskqmeeeavrlfiewlkng 29
Search completed: Mon Oct 4 15:23:58 1999
Job time: 8 secs.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Oct 4 15:22:56 1999; MasPar time 4.19 Seconds 209.327 Million cell updates/sec Run on:

".ular output not generated.

>MOHAM-312-CLAIM82A.PBP (1-31) from moham312177.pep 227 1 hgegtftsdlskqmeeeavrlfiewlknggp 31 Litle: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 34.930; Variance 58.252; scale 0.600 swiss-prot37 1:swissprot Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	1.24e-30	4.43e-29	1.46e-09	2.28e-09	2.07e-08	4.95e-08	4.95e-08	7.64e-08	1.18e-07	2.79e-07	2.79e-07	2.79e-07	2.79e-07	2.79e-07	2.79e-07	2.79e-07	2.79e-07	2.79e-07	4.28e-07	6.56e-07	2.34e-06	5.44e-06	1.90e-05
	Description	EXENDIN-4 PRECURSOR.	EXENDIN-3.	GLUCAGON PRECURSOR (FR	GLUCAGON PRECURSOR (FR	GLUCAGON-LIKE PEPTIDE	GLUCAGON PRECURSOR (FR	GLUCAGON PRECURSOR.	GLUCAGON II PRECURSOR.	GLUCAGON PRECURSOR (FR	GLUCAGON.	GLUCAGON PRECURSOR (FR	GLUCAGON PRECURSOR.	GLUCAGON I PRECURSOR.	GLUCAGON.	GLUCAGON.	GLUCAGON II.							
SUMMAKLES	ID	EXE4_HELSU	EXE3_HELHO	GLUC_RANCA	GLUC_ICTPU	GLUM_ANGAN	GLUC_LEPSP	GLUC_CARAU	GLU2_LOPAM	GLUC_ONCKI	GLUC_SCYCA	GLUC_PIG	GLUC_MOUSE	GLUC_HUMAN	GLUC_CAVPO	GLUC_OCTDE	GLUC_MESAU	GLUC_RAT	GLUC_BOVIN	GLUC_CHICK	GLU1_LOPAM	GLUC_CHIBR	GLUC_TORMA	GLU2_ORENI
	DB	-	Н	Н	H	-4	Н	Н	Н	Н	۲-1	, ,	Н	н	Н	-4	н	Н	Н	-	н	Н	н	Н
	Query Match Length DB	87	39	103	71	30	78	121	122	68	58	158	180	180	180	180	180	180	180	151	124	29	29	33
æ	Query	100.0	6.96	55.9	55.5	53.3	52.4	52.4	52.0	51.5	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.2	49.8	48.5	47.6	46.3
	Score	227	220	127	126	121	119	119	118	117	115	115	115	115	115	115	115	115	115	114	113	110	108	105
	Result No.	1	7	٣	4	5	Ø	7	6 0	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

Query Match 100.0%; Score 227; DB 1; Length 87; Best Local Similarity 100.0%; Pred. No. 1.24e-30;

2.866.05 2.866.05 11.476.04 12.206.04 2.206.04 3.206.04 7.306.04 7.306.04 1.638.02 1.638.02 1.638.02 1.638.02 1.638.02 1.638.02 1.638.02 1.638.02 1.64.476.01 4.476.01	4.47e-01 4.47e-01 4.47e-01 6.37e-01
PRECURSOR PRECURSOR I. I. I. MERASE BETA MERASE BETA MERASE BETA MERASE BETA MERASE BETA MERASE BETA MICAL 47.8 K ICAL 47.8 K	GASTRIC INHIBITORY POL GASTRIC INHIBITORY POL V-TYPE SODIUM ATP SYNT SECRETIN PRECURSOR.
GLUC_PLAPE GLUC_CART GLUC_CART GLUC_CART GLUC_CALMI GLUC_CALMI GLUC_CALMI GLUC_ARDE GRUC_ARDE GL	GIP_RAT GIP_HUMAN NTPC_ENTHR SECR_RAT
296 296 296 297 2112 2112 2142 404 170 170 170 170 170 170 170 170 170 170	144 153 328 134
444444444444 004466664446 00446666444 0044666444 00444666444 00444466 00444466 00444466 0044666 004466 0046666 004666 0046666 0046666 0046666 0046666 0046666 00466666 0046666 0046666 0046666 0046666 00466666 0046666 0046666 0046666 00466666 0046666 0046666 00466666 00466666 00	34.8 34.8 34.8
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ALIGNMENTS

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PFAM; PF00123; hormone2; 3. HSSP; P01274; 1GCN.
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MEDLINE; 87156787.
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GLUC_ICTPU
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NON_TER
SEQUENCE
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PEPTIDE
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P15438; P15439; P15440;
D1-APR-1390 (REL. 14, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR (FRAGMENTS).
RANA CATESBELANA (BULL FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
                                                                                                                                                                                                                                       ENG J.; ANDERW P.C., KLEINMAN W.A., SINGH L., RAUFMAN J.-P.;
"Purification and structure of exendin-3, a new pancreatic
J. Purification and structure of exendin-3, a new pancreatic
J. BIOL. CHEM. 265:20259-20262(1990).
-!- FUNCTION: HAS A VIP/SECRETIN-LIKE BIOLOGICAL ACTIVITY. INTERACTS
WITH THE EXENDIN RECEPTOR.
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
PIR; A23674: HWGH3Z.
PROSITE; PROSIZED: GLUCAGON; 1.
PREAM: PF00123; hormone2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE, 88257102.
POLLOCK H.G., HAMILTON J.W., ROUSE J.B., EBNER K.E., RAWITCH A.B.;
Isolation of peptide hormones from the pancreas of the bullfrog
(Rana catesbelana). Amino acid sequences of pancreatic polypeptide,
J. BIOL. CHEM. 263:9746-9731(1988).
I. BIOL. CHEM. 263:9746-9731(1988).
THE BLOOD SUGAR LEVEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-!- X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH OTHER SPECIES SEQUENCES.
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                          HELODERMA HORRIDUM HORRIDUM (MEXICAN BEADED LIZARD).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAURIA; SQUAMATA;
SCLEROGLOSSA; ANGUIMORPHA; HELODERMATIDAE; HELODERMA
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0
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Pred. No. 4.43e-29;
2; Mismatches 0; Indels
    Indels
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0
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-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
PIR; B28091; GCFGB.
PROSITE; PS00260; GLUCAGON; 3.
                                                                                                       01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
EXENDIN-3.
                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES 39 39 AMIDATION.
SEQUENCE 39 AA; 4204 MW; AB598FD3 CRC32;
                                                                                            39 A.A.
  Mismatches
                     48 HGEGTFTSDLSKQMEEEAVRLFIEWLKNGGP 78
                                  1 HSDGTFTSDLSKQMEEEAVRLFIEWLKNGGP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 hgegtftsdlskqmeeeavrlfiewlknggp 31
                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                      GLUCAGON FAMILY; VENOM; AMIDATION
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0
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Best Local Similarity 93.5%;
Matches 29; Conservative
 Conservative
                                                                                           STANDARD;
                                                                                                                                                                                                                    TISSUE-VENOM;
MEDLINE; 91056067.
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31;
                                                                             EXE3_HELHO
P20394;
                                                                                                                                                                                                          SEQUENCE
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ICTALUNGS PUNCTATUS (CHANNEL CATFISH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; SILURIFORMES; ICTALURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 85157536.
ANDREWS P.C., RONNER P.;
"Isolation and structures of glucagon and glucagon-like peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           catfish pancreas...;
J. Balch. CHEM. 260:3910-3914(1985).
-1- FUNCIION: PROMOTES TARROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.
-1- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-1- X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH AMERICAN GOOSEFISH SEQUENCES.
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOOSEIN, N.M., MAHRENHOLZ A.M., ANDREWS P.C., GURD R.S.; "Biological activities of catfish glucagon and glucagon-like peptide."; BIOCHEM. BIOCHEM. BIOCHEM. BIOCHEM.
                                                                                                                                                                                  Length 103;
                                               GLUCAGON-36 (OXYNTOMODULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 126; DB 1; Length 71;
Pred. No. 2.28e-09;
9; Mismatches 6; Indels
                                                                                                                                                                                                                          Indels
                        29 GLUCAGON.
36 GLUCAGON-36 (OXYNTOMODUL
70 GLUCAGON-LIKE PEPTIDE 1.
71 GLUCAGON-LIKE PEPTIDE 2.
51 11719 MW; D43EDFC9 CRC32;
                                                                                                                   ď
                                                                        GLUCAGON-LIKE PEPTIDE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLUCAGON.
GLUCAGON-LIKE PEPTIDE.
E -> D (IN REF. 2).
                                                                                                                                                                             Score 127; DB 1; Le
Pred. No. 1.46e-09;
8; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1986 (REL. 03, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                 71 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C49ED93A CRC32;
                                                                                                                                                                                                                                                              39 HADGIFTSDMSSYLEEKAAKEFVDWLIKGRP 69
                                                                                                                                                                                                                                                                                         38 HADGTYTSDVSSYLQEQAAKDFITWLKSGQP 68
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00260; GLUCAGON; 2. PFAM; PF00123; hormone2; 2. HSSP; P01274; 1GCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 71
53 53
71 71
71 AA; 8173 MW;
                                                                                                                                                                         Query Match
Best Local Similarity 51.6%;
Matches 16; Conservative
GLUCAGON FAMILY; HORMONE.
PEPTIDE 1 29
PEPTIDE 36
PEPTIDE 39 70
NON_CONS 70 71
PEPTIDE 71 103
SEQUENCE 103 AA; 11719 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 55.5%;
Best Local Similarity 51.6%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLUCAGON FAMILY; HORMONE
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Best Loc
Matches
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ID GI
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MEDLINE; 91340068.

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MEDLINE; 91340068.

MEDLINE; 91340068.

The primary structure of glucagon-like peptide but not insulin has consorved between the American eel, Anguilla rostrata and the trucpean eel, Anguilla anguilla.";

The primary structure of glucagon-like peptide but not insulin has been conserved between the American eel, Anguilla rostrata and the trucpean eel, Anguilla anguilla.";

The Deen conserved between the American eel, Anguilla rostrata and the trucpean eel, Anguilla anguilla.";

The English of The Trucpean eel, Anguilla rostrata and the trucpean eel, Anguilla rostrata and the trucpean eel, Anguilla anguilla.";

PER SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

PIR, 561125; C61125.

PIR, 561125; C61
                                                                                                                                                                                                                                                    ANGUILLA ANGUILLA (EUROPEAN FRESHWATER EEL), AND
ANGUILLA ROSTRATA (AMERICAN EEL).
EUKARYOTA: METAZOA: CHORDAMA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; ANGUILLIFORMES; ANGUILLIDAE; ANGUILLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEPISOSTEUS SPATULA (ALLIGATÓR GAR) (ATRACTOSTEUS SPATULA).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
SEMIONOTIFORMES; LEPISOSTEIDAE; LEPISOSTEUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation and structures of alligator gar (Lepisosteus spatula) insulin and pancreatic polypeptide."; GEN. COMP. ENDOCRINOL. 67:375-382(1987).
-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation of alligator gar (Lepisosteus spatula) glucagon, oxyntomodulin, and glucagon-like peptide: amino acid sequences of oxyntomodulin and glucagon-like peptide."; eBND CRINOL. 69:133-140(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLLOCK H.G., KIMMEL J.R., HAMILTON J.W., ROUSE J.B., EBNER K.E.,
LANCE V., RAWITCH A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLLOCK H.G., KIMMEL J.R., EBNER K.E., HAMILTON J.W., ROUSE J.B.,
LANCE V., RAWITCH A.B.;
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Pred. No. 2.07e-08;
9; Mismatches 6; Indels
                                                                                                                        01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
GLOCAGON-LIKE PEPTIDE (GLP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLUC_LEPSP STANDARD; PRT; 78 AA. p09566.

10, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27E8C37D CRC32;
                                                               30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HAEGTYTSDVSSYLQDQAAKEFVSWLKTG 29
                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLUCAGON PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY SEQUENCE OF 1-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 AA; 3376 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLUCAGON FAMILY; AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.3%;
Best Local Similarity 48.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-36 AND 45-78.
TISSUE-PANCREAS;
                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 88196798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 88030594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IISSUE-PANCREAS
                                                        GLUM_ANGAN
P41521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                              RESULT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
CYPRINIDAE; CYPRININAE; CARASSIUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YUEN T.T.H., MOK P.Y., CHOW B.K.C.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL. SIGNAL 1 \\ 21 \\ 21
                                                                                                                                                                                                                                                                                                                                                   Gaps
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GRPP (GLICENTINE RELATED POLYPEPTIDE),
GLUCAGON.
-!- X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH AMERICAN
                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                            Score 119; DB 1; Length /0;
Pred. No. 4.95e-08;
...matches 6; Indels
                                                                                                                                                                                                        GLUCAGON-36 (OXYNTOMODULIN). GLUCAGON-LIKE PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 119; DB 1; Length 121 Pred. No. 4.95e-08; 9; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 121 GLUCAGON-LIKE PEPTIDE.
121 AA; 13527 MW; DDB662CE CRC32;
                      GOOSEFISH SEQÜENCES.
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
PIR; S06339; GCGXA.
PROSITE; PS00260; GLUCAGON; 2.
PROSITE; PS00123; hormone2; 2.
HSSP; P01274; IGCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR.
                                                                                                                                                                                                                                                           509ED9D3 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLUCAGON
                                                                                                                                                                                                                                                                                                                                                                                               45 HADGIYISDVSSYLQDQAAKKFVTWLKQG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00260; GLUCAGON; 2. PFAM; PF00123; hormone2; 2. HSSP; P01274; IGCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
ID GLU2_LOPAM STANDARD;
AZ P04.092;
DT 01-NOV-1986 (REL. 03, CREATED)
                                                                                                                                                                                       1 29
1 36
45 78
78 AA; 8990 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.48;
                                                                                                                                                                                                                                                                                                     52.4%;
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Conservative
                                                                                                                                                                                                                                                                                                                             Best Local Similarity 44.8%;
                                                                                                                                                                                                                                                                                                                                                   13; Conservative
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                                                                                                                                                              GLUCAGON FAMILY; HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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P79695;
                                                                                                                                                                                                                                   PEPTIDE
SEQUENCE
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PEPTIDE
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158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HSEGTFTSDYSKYMDNRRAKDFVQWLMN 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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PROSITE; PS00260; GLUCAGON; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A26992; GCDF.
PROSITE; PS00260; GLUCAGON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.7%;
larity 53.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             7810 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    th 51.5%;
Similarity 41.4%;
12; Conservative
                                                                                                                                                                                                                                                                                             PFAM; PF00123; hormone2; 2
HSSP; P01274; IGCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00123; hormone2; 1. HSSP; P01274; 1GCN.
                                                                                                                                                                                                                                                                                                                                      GLUCAGON FAMILY; HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               68 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 10
GLUC_SCYCA
P09687;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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ID GLUC_PIG
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NON_TER
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        HHHH COCCOCCOCKARA HHHHH COCCOCCOCKARA HHHHH COCCOCCOCKARA HHHHH COCCOCCOCKARA HHHHH COCCOCKARA HHHH COCCOCKARA HHHH COCCOCKARA HHH COCCOCKARA HHH COCCOCKARA HHH COCCOCKARA HHH COCCOCKARA HH COCCOCKARA HA COCCOCCACA HA COCCOCCACA HA COCCOCCACA HA COCCOCCACA HA COCCOCCACA HA COCCOCCACA HA COCCACA HA CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1986 (REL. 03, LAST SEQUENCE UPDATE)
115-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUCAGON II PRECURSOR.
LOPHIUS AMERICANUS (AMERICAN GOOSEFISH) (ANGLERFISH).
EUKARYOTA; METALOA; CHORDATA; VERYEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PARACANTHOPTERYGII; LOPHIIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES;
SALMONIDAE; ONCORHYNCHUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
MEDINE; 86234328.
PLISEISKAYA E., POLLOCK H.G., ROUSE J.B., HAMILTON J.W., KIMMEL J.R.,
GORBARAN A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.
-1- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                               MODE B.D., ANDREWS.

"Specific glucagon-related peptides isolated from anglerfish islets are metabolic cleavage products of (pre)proglucagon-II.";

PEPTIDES 7:331-339(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                        LUND P.K., GOODMAN R.H., MONTMINY M.R., DEE P.C., HABENER J.F., "Anglerfish islet pre-proglucagon II. Nucleotide and corresponding amino acid sequence of the CDNA.";
J. BIOL. CHEM. 258:2289(2884(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRPP (GLICENTINE RELATED POLYPEPTIDE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 80 GLUCAGON II.
89 119 GLUCAGON-LIKE PEPTIDE
122 AA; 14171 MW; DFE63061 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 118; DB 1; 1
Pred. No. 7.64e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLUC_ONCKI STANDARD; PRT; 68 AA.
P07449;
01-APR-1988 (REL. 07, CREATED)
01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR (FRAGMENT).
ONCORHYNCHUS KISUTCH (COHO SALMON).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Mismatches
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PIR; A05150; GCAF2.
PROSITE; PS00260; GLUCAGON; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.0%;
Best Local Similarity 44.8%;
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HSSP; P01274; 1GCN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; V00632; G64022; -.
                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 83135785.
                                                                                                                                                                                                                                                                                                                                  MEDLINE; 86286913
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MEDINE; 87190953.
MEDINE; 87190953.
MEDINE; 87190953.
"Primary structure of glucagon from the gut of the common dogfish (SCYLIOTAIDUS CANICULA)."
"FESTALOTAIDUS CANICULA)."
"FEST LETT. 214:50-56(1987).
"FEB SLOOD SUGAR LEVEL.
"ITE BLOOD SUGAR LEVEL.
"ITE DATO SUGAR LEVEL.
"IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
"SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                      Gaps
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EUKARYOTA, METALOA; CHORDATA; VERTEBRATA; CHONDRICHTHYES;
ELASMOBRANCHII; CARCHARHINIFORMES; SCYLIORHINIDAE; SCYLIORHINGS.
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Pred. No. 2.79e-07;
7; Mismatches 6; Indels
                                                                                                                                      Length 68;
                                                                                                                                Score 117; DB 1; Length 68;
Pred. No. 1.18e-07;
12; Mismatches 5; Indels
GLUCAGON.
GLUCAGON-LIKE PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-JAN-1990 (REL. 13, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLUCAGON FAMILY; HORMONE.
SEQUENCE 29 AA; 3529 MW; RCFE41FB CRC32;
                                                                               402B55D1 CRC32;
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MOHAM-312-CLAIM82A.PEP.rsp

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Score 115; DB 1; Ler
Pred. No. 2.79e-07;
Best Local Similarity 55.2%; Pred. No. 2.79e-07;
Matches 16; Conservative 6; Mismatches 7;
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13-A0C-1987 (REL. 05, LAST SEQUENCE UPDATE)
15-EC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR.
                                                                                                                                                                                                             LT 12
GLOC_MOUSE STANDARD; PRT; 180 AA.
GLOC_LOGS:
01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1999 (REL. 36, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR.
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                                                                             78 HAEGTFTSDVSSYLEGQAAKEFIAWLVKG 106
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50 GR
81 GL
128 GL
178 GL
20906 MW;
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PFAM; PF00123; hormone2; 3.
HSSP; P0174; 1GON.
GLUCAGON FAMILY; HORMONE; CLEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.7%;
llarity 55.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           MUS MUSCULUS (MOUSE).
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92
146
180 AA;
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P01275;
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SEQUENCE
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PEPTIDE
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BUHL T., THIM L., KOPOD H., ORSKOV C., HARLING H., HOLST J.J.;

BUHL T., THIM L., KOPOD H., ORSKOV C., HARLING H., HOLST J.J.;

"Naturally occurring products of proglucagon 111-160 in the porcine and human small intestine.";

J. BIOL. CHEM. 263:8621-8624(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLYPEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SASAKI K., DOCKERILL S., ADAMIAK D.A., TICKLE I.J., BLUNDELL T.L., "X-ray analysis of glucagon and its relationship to receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 33-61.
BROWER W.W., SINN L.G., BEHRENS O.K.;
The amino acid sequence of glucagon. V. Location of amide groups, acid degradation studies and summary of sequential evidence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE; 89327238.
SYSKOV C., BERSANI M., JOHNSEN A.H., HOEJRUP P., HOLST J.J.;
"Complete sequences of glucagon-like peptide-1 from human and pig
small intestine.";
                                                                                                                                                              SUS SCROFA (PIG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES;
                                                                                                                                                                                                                                                                                           MEDLINE; 81248172.
THIM L., MODY A.J.;
"The primary structure of porcine glicentin (proglucagon).";
REGUL. PEPT. 2:139-150(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The amino acid sequence of porcine glicentin."; PEPTIDES 2 SUPPL. 2:37-39(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - SIMILARITY: BELONGS TO THE GLUCAGON FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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                                                 1-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
5-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00260; GLUCAGON; 3.
                                 21-JUL-1986 (REL. 01, CREATED)
                                                                                                         GLUCAGON PRECURSOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00123; hormone2;
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56
158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 78-107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 82221776.
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PDB; 1GCN; 30-SEP
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TISSUE-PANCREATIC ISLETS;

MEDLINE; 95.47722.

MEDLINE; 95.47722.

MEDLINE; 95.47722.

MEDRINES OF M.E., ELLERESON C.D., KLEIN K., ZHOU Y., LINBERG I., MCONALD J.K., MACKIN R.B., NOE B.D.;

Processing of mouse proglucagon by recombinant prohormone convertase I and immunopurified prohormone convertase 2 in vitro.";

J. BIOL, CHEM. 270:10136-10146(1995).

-I- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPLIDS, AND RAISES THE BLOOD SUGAR LEYEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.
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GRPP (GLICENTINE RELATED POLYPEPTIDE).
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-i- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
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GLUCAGON-LIKE PEPTIDE 1.
GLUCAGON-LIKE PEPTIDE 2.
0B21B7BA CRC32;
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HOMO SAPIENS (HUMAN).
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STURM N.S., LIN Y., BURLEY S.K., KRSTENANSKY J.L., AHN J.M.,
AZIZEH B.Y., TRIVEDI D., HRUBY V.J.;
"Structure-function studies on positions 17, 18, and 21 replacement
analogues of glucagon: the importance of charged residues and salt
bridges in glucagon blological activity.";
J. MED. CHEM. 41:A593-2700(1998).
I- FUNCTION: PROMOTES HYDROLISIS OF GLYCOGEN AND LIPIDS, AND RAISES
THE BLOOD SUGAR LEVEL.
INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 83271477.
BELL G.I., SANCHEZ-PESCADOR R., LAYBOURN P.J., NAJARIAN R.C.; "Exon duplication and divergence in the human preproglucagon gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRPP (GLICENTINE RELATED POLYPEPTIDE).
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    CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 53-81.

THOMSEN J., KRISTIANSEN K., BRUNFELDT K., SUNDBY F.;

"The amino acid sequence of human glucagon.",

FEBS LETT. 21:315-319(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLUCAGON-LIKE PEPTIDE
                                                                                                                                                             MEDLINE, 88330860.
DRUCKER D.J., ASA S.;
"Glucagon gene expression in vertebrate brain.";
J. BIOL. CHEM. 263:13475-13478(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure of the human glucagon gene."; NUCLEIC ACIDS RES. 14:4719-4730(1986).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRA
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. BIOL. CHEM. 264:12826-12829(1989)
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EMBL, X03991, -.
EMBL, V01515, G31778, -.
EMBL, V01515, E28349, ALT_SEQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE, 86259053.
WHITE J.W., SAUNDERS G.F.;
"Structure of the human gli
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PDB; 1BH0; 18-NOV-98.
GLUCAGON FAMILX; HORMONE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NATURE 304:368-371(1983).
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PIR; A24377; GCHU.
PIR; S23309; S23309.
                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 88330860.
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MIM; 231530; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 86017849.
MEDLINE; 86017849.
COLLON J.M., HANSEN H.F., SCHWARTZ T.W.;
Primary structure of glucagon and a partial sequence of oxyntomodulin (glucagon.37) from the guinea pig.";
REGUL. PEPT. 11:309-320(1985).
THE BLOOD SUGAR LEVEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 86248118.
SELOS, WEISH M., BELL G.I., CHAN S.J., STEINER D.F.;
"Mutations in the guinea pig preproglucagon gene are restricted to specific portion of the prohormone sequence.";
FEBS LETT. 203:25-30(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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MEDLINE: 86165412.
HUGNG C.G., ENG J., PAN Y.-C.E., HULMES J.D., YALOW R.S.;
"Guinea pig glucagon differs from other mammalian glucagons.";
DIABETES 35:508-512(1986).
                                                                                          .;
                                                                                                                                                                                                                                                                                                                           CAVIA PORCELLUS (GUINEA PIG).
EUKARYOTA, BETAZOA, CHORDATA, VERTEBRATA; MAMMALIA, EUTHERIA,
RODENTIA, HYSTRIGOSMATHI, CAVIIDAE; CAVIA.
                                                             Length 180;
                                                                                            Indels
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   GLUCAGON-LIKE PEPTIDE 2.
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GLUCAGON-LIKE PEPTIDE 2.
9B724097 CRC32;
                                                          Score 115; DB 1; Le
Pred. No. 2.79e-07;
6; Mismatches 7;
                 82 K -> N (IN REF. 3).
20909 MW; DEE43985 CRC32;
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13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
11-ERB-1996 (REL. 33, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR.
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                                                                                                                                        GLUCAGON
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PROSTIE: PSOD260; GLUCAGON; 4.
PFAM; PF00123; hormone2; 3.
HSSP; P01274; 1GCN.
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                                                          Query Match
Best Local Similarity 55.2%;
Matches 16; Conservative
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146 1
82
180 AA;
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Length 180;

DB 1;

50.7%; Score 115;

Query Match

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PRIS, C36118, CGRUD.
PROSTUE: PS00260; GUUCAGON: 4.
PROSTUE: PS00123; hormone2; 3.
HSSP: P01274; 1GCN.
AGLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL; AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE, 9115592.

NISHI M., STEINER D.F.;

NISHI M., STEINER D.F.;

NISHI M., STEINER D.F.;

NISHI M., STEINER D.F.;

Cloning of complementary DNAs encoding islet amyloid polypeptide, insulin, and glucagon precursors from a New World rodent, the degu, Octodon degus.";

AGL. ENGORINGL. 4:1192-1198(1990).

HOL. ENGORINGL. 4:1192-1198(1990).

THE BLOOD SUGAR LEVEL.
                                      Gaps
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81 GLUCAGON.
127 GLUCAGON-LIKE PEPTIDE 1.
61UCAGON-LIKE PEPTIDE 2.
1178 ANIDATION (G-128 PROVIDE AMIDE GROUP).
21165 MW; 4Alfsce3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-:- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; HYSTRICOGNATHI; OCTODONTIDAE; OCTODON.
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Pred. No. 2.79e-07;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR.
                                                                                                                                                                                                                                                                                                        180 AA.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Oct 4 15:23:19 1999; MasPar time 10.07 Seconds 168.071 Million cell updates/sec Run on:

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>MOHAM-312-CLAIM82A.PEP (1-31) from moham312177.pep 227 1 hgegtftsdlskqmeeeavrlfiewlknggp 31 Late: Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues

Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 33.361; Variance 61.380; scale 0.544 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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sult No.	Score	Query Match	Query Match Length	DB	a a	Description	Pred. No.
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o	108	47.6	149	13	012955	PROGLUCAGON.	3.10e-05
10		47.6	204	13	012956	PROGLUCAGON.	3.10e-05
11	95	41.9	2127	14	057294	L PROTEIN, RNA DEPENDE	4.25e-03
12		37.9	552	σ	038064	REPLICASE.	1.08e-01
13		34.4	379	?	085863	HYPOTHETICAL 42.3 KD P	1.66e+00
7	77	33.9	414	Ŋ	021764	ROSH5.4 PROTEIN.	2.31e+00
15	9.2	33.5	300	Н	059151	300AA LONG HYPOTHETICA	3.20e+00
16	16	33.5	1015	~	067146	FORMATE DEHYDROGENASE	3.20e+00
17	9.2	33.5	1086	4	013423	NICOTINAMIDE NUCLEOTID	3.20e+00
8	1 76	33.5	1086	4	016796	NAD(P) TRANSHYDROGENAS	3.20e+00
19	9.2	33.5	1086	11	061941	NICOTINAMIDE NUCLEOTID	3.20e+00
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ALIGNMENTS

042143 PRELIMINARY; PRT; 266 AA. 042143; 01-134-1998 (TREMBLREL. 05, CREATED) 01-140-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE) 01-154-1998 (TREMBLREL. 06, LAST SEQUENCE TROW N.A. MESOBATRACHIA; PIPOIDEA; PIPIDAE; TROPODINAE; TROPODIS. 11 11 SEQUENCE TROW N.A. MESOBATRACHIA; PIPOIDEA, PIPIDAE; TROPODINAE; TROPODIS. 11 11 SAIL TOOLOGIC TOOLOGIC. 11 SEQUENCE TROW N.A. MESOBATRACHIA; PRODICES. 15 SEQUENCE 266 AA; 30951 MM; E6139A25 CRC32; 15 SEQUENCE 266 AA; 30951 MM; E6139A25 CRC32; 15 SEQUENCE 266 AA; 30951 MM; E6139A25 CRC32; 16 SEQUENCE 266 AA; 30951 MM; E6139A25 CRC32; 17 MATCH 11 1 1 1 1 1 1 1 1 1	042143 PRELIMINARY; PRT; 266 AA. 042143; 261-3AN-1998 (TREMELREL. 05, CREATED) 01-3AN-1998 (TREMELREL. 05, LAST SEQUENCE U 01-NOV-1998 (TREMELREL. 05, LAST SEQUENCE U 1-NOV-1998 (TREMELREL. 06, LAST ANNOTATION XENOPUS LAEVIS (AFRICAN CLAMED FROG). EUKARYOTA, METAZOA; CHORDAIA; VERTEBRATA; A MESCBARRACHIA; PIPOIDEA; PIPIDAE; XENOPODIN [1]	POATE
-JAN-1998 (TREMBLREL. 05, CREATED) -JAN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE) -JAN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE) -JAN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE) OGLUCAGON 1. NOOPUS LAEVIS (AFRICAN CLAWED FROG.) NARRYOTA, WETAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; SEGNBATRACHIA; PIPOIDEA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOF SELINE; 97368292. SELINE; 97368292. SELINE; 97368292. SELINE; 97368292. SELINE; 97368292. THEELER M.B.; TANDODERIARE P.L.; HEELER M.B.; ARTHORADARA, WEN Y., BRUBAKER P.L.; HEELER M.B.; ARTHORADARA, WEN Y., BRUBAKER P.L.; HEELER M.B.; ALCAD. SCI. US.A. 94:7915-7920(1997). ACC. NATL., ACAD. SCI. WA. A. ACC. NATL., ACC. NA.A. BERELMINARY, PERLIMINARY, PRETERRATE, NAMPHIBIA; BESCHATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPLINE; BURNARO, A.A. BURNARO, A.A. ACC. NATL., ACC. ACC. A.A. BURNARO, A.A. ACC. NATL., ACC. A.A. ACC. NATL., ACC. A.A. BURNARO, A.A. ACC. NATL., ACC. A.A. A	01-JAN-1998 (TREMBLREL. 05, CREATED) 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE U 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION PROGLUCAGON I. XENOPUS LABVIS (AFRICAN CLAWED FROG). EURANYOTA; METAZOA; CHORDATA; VERTEBRATA; A MESOBATRACHIA; PIPOIDEA; PIPOIDEA; YERUEBRATA; A 111 113	PDATE
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TRARYOTE, METAZON, CHORDATA, VERTEBRATA, AMPHIBIA, SCOBATRACHIA, PIPOIDEA, PIPIDAE; XENOPODINAE, XENOPOLINE, SCOBATRACHIA, PIPOIDEA, PIPIDAE; XENOPODINAE, XENOPOLINE, STRUDINE, 9736829. WILL ME, SATKUNARAJAH M., WEN Y., BRUBAKER P.L., IEELER M.B.; SATKUNARAJAH M., WEN Y., BRUBAKER P.L., IEELER M.B.; SATKUNARAJAH M., WEN Y., BRUBAKER P.L., IEELER M.B.; STOPETICS, TO SCI. U.S.A. 94:7915-7920(1997). WOC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997). WOSITE, PRO0123; HORMOROS, 5. RAM; PF00123; HORMOROS, SENORDINAE; XENOFOLINAE; XENO	MESOBATRACHIA, METAZOA, CHORDATA, VERTEBRATA, A MESOBATRACHIA, PIPOIDEA, PIPIDAE, XENOPODIN [1]	
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IEELER M.B.; RELER M.B.; RELEACOPUS proglucagon gene encodes novel GLP-1-11 Stall incurpic properties.; CC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997). ROC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997). ROSITE; PE00432; G1040AG0N; 5. RAM; PF00123; hormone2; 5. ROGITE; PE00123; hormone2; 5. ROGITE; PE00123; hormone2; 5. ROGITE; PE00123; hormone2; 5. ROGITE; PE00123; hormone2; 5. ROGICAC SIMILARITY 61.3%; Pred. No. 1.68e-13; Leng. Local Similarity 61.3%; Pred. No. 1.68e-13; Leng. Local Similarity 61.3%; Pred. No. 1.68e-13; Leng. PREDIMINARY; PRED. NO. 1.68e-13; Ill. ROGIUCAGON II. HILL IIIINARY; RRICHEREREL OS, LAST SEQUENCE UPDATE) ROGIUCAGON II. REMBLREL. OS, CREATED) L. JAN-1998 (TREMBLREL. OS, LAST SEQUENCE UPDATE) ROGIUCAGON II. REPASON: CHONDATA; VERTEBRATA; AMPHIBIA; ESOBATRACHIA; PIPOIDEA; PIPIDAE; KENOPODINAE; XENOI	(, SATKUNARAJAH M., WEN Y.,	
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) PROGLUCAGON II. XENOPUS LAEVIS (AFRICAN CLAWED FROG). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS. [1] SEOURNCE FROM N.A.	(TREMBLREL. 05, CREAT	
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) PROGLUCAGON II. XENOPUS LAEVIS (AFRICAN CLAWED FROG). EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, AMPHIBIA, BATRACHIA, ANDRA MESOBATRACHIA, PIPOIDEA, PIPIDAE, XENOPODINAE; XENOPUS. [1] SEOURNE FROM N.A.	CTREMETERI. 05 LAST	PDATE)
PROGLUCAGON II. XENOPUS LAEVIS (AFRICAN CLAWED FROG). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS. [1] SROHENCE FROM N.A.	(TREMBLREL, 08, LAST	UPDATE)
ANDOPOS LAEVIS (AFRICAN CLAWED FROG). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS. [1] SROHENCE FROM N.A.	11 11	
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS. [1] SROHENCE FROM N.A.	XENOPUS LAEVIS (AFRICAN CLAMED FROG).	
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS. [1] SECURICE FROM N.A.	EIKARYOTA: METAZOA: CHORDATA: VERTEBRATA: A	MPHIBIA; BATRACHIA; ANURA
[1] SROTENCE FROM N.A.	MESOBATRACHIA: PIPOIDEA: PIPIDAE: XENOPODIN	AE: XENOPUS.
SECUENCE FROM N.A.		
	A N MORE HONEITORS	

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PFAM; PF00123; hormone2; 2.
NON_TER 1 1 1
SEQUENCE 72 AA; 8293 MW;
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Best Local Similarity 44.8%;
Matches 13; Conservative
                                                                                                                                                     Query Match 52.9%;
Best Local Similarity 44.8%;
Matches 13; Conservative
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091971;
01-NOV-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
GLUCAGON I.
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091408
091408;
01-NOV-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0
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01-NOV-1998 (TREMBLREL. O
01-NOV-1998 (TREMBLREL. O
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NON_TER
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EUKLRYCTA; METAZOA; CHORDATA; VERIEBRAIA; ACTINOPIERYGII; NEOPIERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPIERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERÚGII; NEOPTERYGII;
TELEGSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                                     "The Xenopus proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-PANCREAS;
MEDLINE; 95295739.
IRWIN D.M., WONG J.;
IRWIN D.M., WONG J.;
Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
MOL. ENDOCRINOL. 9:267-277(1995).
BABL; U19913; G736661; -.
BERM; PF00123; hormone2; 2.
NON_TER 1 1
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"Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
MOL. ENDOCRINOL. 9:267-277(1995).
EMBL; S78474; E206590; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                        IRWIN D.M., SATKUNARAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A., HHEELER M.B.;
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01, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 151; DB 13; L. Pred. No. 6.15e-13; 8; Mismatches 5;
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Pred. No. 2.67e-07;
11; Mismatches 5;
                                                                                                                                                 insulinotropic properties.",
PROC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997)
EMBL; AF004433; G2305018; -.
PROSITE: PSO000; GLUCAGON; 3.
PRAM; PF00123; hormone2; 4.
SEQUENCE 219 AA; 25271 MW; 45C42A88 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 AA; 7680 MW; 62C576E2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 HADGIYISDVSIYLQDQAAKDFVSWLKSG 61
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08,
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Best Local Similarity 58.1%;
Matches 18; Conservative
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13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | TESULT | 3 | PRELIMINARY; | AC | 091188 | PRELIMINARY; | AC | 091188 | DT | 01-NOV-1996 (TREMBLREL. 01 | DT | 01-NOV-1996 (TREMBLREL. 02 | DT | 01-NOV-1998 (TREMBLREL. 03 | DE | GLUCAGONN (FRAGMENN) | CLOCAGNN (FRAGMEN
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    97368292
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ID 091409
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; KEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
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EUKARYOIA: METAZOA; CHORDATA; VERTEBRATA; ACTINOPIERYGII; NEOPIERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
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TISSUB-INFESTINE, DISTAL PORTION;
MEDLINE; 95295739.
MEDLINE; 95295730.

"Trout and chicken proglucagon: alternative splicing generates mrna transcripte seconding glucagon-like peptide 2.";
MOL. ENDORRINO. 9:267-277(1995).

EMBL; 019917, G736365; ---
PROSITE; PS00260; GLUCAGON; 3.
PROM; PF00123; hormone2; 3.
SEQUENCE 178 AA; 20034 MW; 2056F963 CRC32;
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRWIN D.M., WONG J.;
"Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
WOL. ENDOCRINOL. 9:267-277(1995).
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                                        Length 72;
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Pred. No. 2.67e-07;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                     Score 120; DB 13; I
Pred. No. 2.67e-07;
11; Mismatches 5;
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OF7AF3EC CRC32;
                                                                                                                                                                                                                                                            72 AA
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                                                                                                                                                   39 HADGIYISDVSIYLQDQAAKDFVSWLKSG 67
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VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES; RHABDOVIRIDAE; LYSSAVIRUS.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAUKIA; SQUAMATA;
SCLEROGLOSSA; ANGUIMORPHA; HELODERMATIDAE; HELODERMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HELODERMA SUSPECTUM (GILA MONSTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAURIA; SQUAMATA;
SCLEROGLOSSA; ANGUIMORPHA; HELODERMATIDAE; HELODERMA.
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057294 PRELIMINARY; PRT; 2127 AA.
057294;
01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST SHONOTATION UPDATE)
L PROTEIN, RNA DEPENDENT RNA POLYMERASE.
                                                                                                     04, CREATED)
04, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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04, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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Pred. No. 3.10e-05;
7; Mismatches 8;
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CHEN Y.E., DRUCKER D.J.;
CHEN Y.E., DRUCKER D.J.;
EMBL 107612; G1916065; -.
PROSITE; PS00260; G10CAGON; 2.
PROSITE; PS00123; hormone2; SEQUENCE 204 AA; 23553 MW; EB50250D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00123; hormone2; 2.
SEQUENCE 149 AA; 17224 MW; F763AB51 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 HADGRYTSDISSYLEGQAAKEFIAWLVNG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
CHEN Y.E., DRUCKER D.J.;
J. BIOL. CHEM. 0:0-0(0).
EMBL: 077611; G1016063; -.
PROSITE; PS00260; GLUCAGON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.6%;
Local Similarity 48.3%;
hes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.6%;
Local Similarity 48.3%;
Les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1LT 10
012956 PRELIMINARY;
0129555;
01-JUL-1997 (TREMBLREL. 0.
01-JUV-1997 (TREMBLREL. 0.
01-NOY-1998 (TREMBLREL. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                     PRELIMINARY;
                                                                                                        01-JUL-1997 (TREMBLREL. 01-JUL-1997 (TREMBLREL. 01-NOV-1998 (TREMBLREL. PROGLUCAGON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
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SEQUENCE FROM :
STRAIN-RC-HL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RABIES VIRUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
RESULT 9
ID 012955
AC 012955;
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11D 055
12D 051
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AC 091189; 092168;

DI 01-NOV-1996 (TREMBLREL. 01, CREATED)

DI 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DI 01-NOV-1996 (TREMBLREL. 03, LAST SEQUENCE UPDATE)

DI 01-NOV-1998 (TREMBLREL. 04, LAST SEQUENCE UPDATE)

DI 01-NOV-1998 (TREMBLREL. 04, LAST SEQUENCE UPDATE)

CAUCAGON II.

SCHOCRHYNOUTS METALOSA TROUT) (SALMO GAIRDNERI).

CC EDIROXYOTR, METALOSA, VERTEBRATA, ACTINOPTERYGII; NEOPTERYGII;

CC TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;

CC ONCCRHYNCHUS.

RN [1]

RP SEQUENCE FROM N.A.

RC ILSSUE-INTESTINESTINES. DISTAL PORTION;

RR SISSUE-INTESTINESTINES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILSSUE-INTEGINE, DISTAL PORTION;
MEDLINE, 95295739.
MEDLINE, 95295739.
"Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
MOL. ENDOCKINOL. 91267-277 (1995).
EMBL: U19914; G736372; -.
EMBL: U19915; G736372; -.
EMBL: U19915; G736372; JOINED.
EMBL: U19915; G736371; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE, 95295739.

IRWIN D.M., WONG J.,

Trout and chicken proglucagon: alternative splicing generates mRNA

Traut and chicken proglucagon-like peptide 2.";

MOL. ENDOCRINOL. 9:267-277(1995).

EMBL: S78477 (999387; --

EMBL: S78477 (999387; --

EMBL: PROSLIE; PS00260; GLUCAGON; 3.

PROSLIE; PS00123; hormone2, 3.

SEQUENCE 206 AA; 23875 MW; 8EC91118 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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       Gaps
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GALLUCA GALLUS (CHICKEN).
BERARYOTA: METAZOA: CHORDATA: VERTEBRATA: ARCHOSAURIA: AVES;
BUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: PHASIANINAE; GALLUS.
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; GALUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.2%; Score 114; DB 13; Length 206; Best Local Similarity 51.7%; Pred. No. 2.94e-06; Matches 15; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
       Indels
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.9%; Score 120; DB 13; Lalarity 44.8%; Pred. No. 2.67e-07; Conservative 11; Mismatches 5;
       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 AA.
       11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 HAEGIYISDIISYLEGQAAKEFIAWLVNG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 HADGTYTSDVSTYLQDQAAKDFVSWLKSG 118
                                                                          HADGIYISDVSTYLQDQAAKDFVSWLKSG 118
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| hgegtftsdlskgmeeeavrlfiewlkng 29
                                                                                                                    PRT;
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Matches 13; Conser
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       13;
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Q91410
Q91410;
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RESULT 1D 099 AC 091 DIT 011 DIT 011 DIT DIT DIT DE PR

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Best Local Similarity 38.5%;
Matches 10; Conservative
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01-NOV-1996 (TREMBLREL. 0
01-AUG-1998 (TREMBLREL. 0
RO5HS. 4 PROTEIN.
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Matches 10; Conservative
                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                    CAENORHABDITIS ELEGANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                  LT 14
021764
021764;
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059151
059151;
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OLSTHOORN R.C.L., GARDE G., DAYHUFF T., ATKINS J.F., VAN DUIN J.;
"Nucleotide sequence of a single-stranded RNA phage from Pseudomonas aeruginosa: kinship to coliphages and conservation of regulatory RNA
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACTERIOPHAGE PP7.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; LEVIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-F199;
ROMINE M.F., STILLWELL L.C., WONG K.-K., THURSTON S.J., SISK B.C.,
ROMINE M.F., STILLWELL L.C., WONG K.-K., THURSTON S.J., SISK B.C.,
"Complete sequence of a 184 kb catabolic plasmid from Sphingomonas
aromaticivorans strain F199.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF079317; G3378295; --.
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SPHINGOMONAS.
                                                                                                                                                                                                                                                            Length 2127;
                                                                                                                                                                                                                                  Score 95; DB 14; Length 212
Pred. No. 4.25e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 86; DB 9; Length 552;
Pred. No. 1.08e-01;
                                                                                  SIGNATION ...
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AB009663; D1024994; -.
EMBL; AB0096601; D1024989; -.
SPOTENCE 2127 AA; 242427 MW; 847321FB CRC32;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
11-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHERICAL 4.2.3 KD PROPEIN.
SPHINGOMONAS AROMATICIVORANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   structures.";
VIROLOGY 206:611-625(1995).
EMBL; X80191; G517241; -.
SEQUENCE 552 AA; 63300 MW; 35D63A16 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              552 AA.
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9 dlskqmeeeavrlfiewlkn 28
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01,
08,
                                                                                                                                                                                                                                                  / Match 41.9%;
Local Similarity 47.6%;
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.9%;
45.0%;
                                                                                                                                                                                                                                                                                                                                                    37 NLNSPLIEDPVRLMLEWLKTG
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Best Local Similarity 45.0%,
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                             SEQUENCE FROM N.A. STRAIN-RC-HL;
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                                                                                                                                                                                                                                                    Query Match
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Q38064
Q38064;
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085863
085863;
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34.4%; Score 78; DB 2; Length 379;

W; PLASMID. 42269 MW; ED0127FC CRC32;

HYPOTHETICAL PROTEIN; SEQUENCE 379 AA; 42

RESULT

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Query Match

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MEDLINE: 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAINES C., BERKS M.,
AINSCOUGH R., ANDERSON K., BAINES C., BERKS M.,
BONFIELD J., BURTON J., CONBELL M., COPSET T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
ACRUDIER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
LIGHTANNG J., LLOYD C., MCWINERAY A., MORTIMORE B., O'CALLAGIAN M.,
ARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
AMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
T. 2.2 MD of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
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KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,
SAKAI M., OGURA K., OTUKA R., NIKAZAWA H., TAKAMITA M., OHFUKU Y.,
SAKAI M., OKURA K., OTUKA Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
AOKI K., NAKAWURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
KIKUCHI H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COULSON A.
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDIIIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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                            1;
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-ANG-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
300AA LONG HYPOTHETICAL TRANSCRIPTION INITIATION FACTOR IIB
Pred. No. 1.66e+00;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 414;
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SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDEJ DATA BANKS.
                                                                                                                                                                                                                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 77; DB 5; Len
Pred. No. 2.31e+00;
9; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATURE 368:32-38(1994).
EMBL, Z48795; E1351719; -.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
SEQUENCE 414 AA; 47188 MW; 73B4DF09 CRC32;
                                                                                                                                                                                                                         414 AA
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                                                                   159 FEAPPSREMAAEMAR-FLEWFAATGP 183
                                                                                                                                                                                                                       PRT;
                                                                                                               ftsdlskqmeeeavrlfiewlknggp 31
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RT "Complete Sequence and Gene Organization of the Genome of a RT Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii Ori."; RL DNR RES 5:55-76(1998).
DR RMEL, AP000006; D1031522; -. DR PROSITE: PS00782; TFIIB; 2.
KW INITIATION FACTOR.
SQ SEQUENCE 300 AA; 34097 MW; 6E17BB64 CRC32;
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Query Match
33.5%; Score 76; DB 1; Length 300;
Best Local Similarity 50.0%; Pred. No. 3.20e+00;
Matches 10; Conservative 7; Mismatches 3; Indels
Db 125 LPKHVEEEAARLYREAVRKG 144
|:|::|||| |: |::||
Qy 10 lskqmeeeavrlfiewlkng 29

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0; Gaps

Search completed: Mon Oct 4 15:23:33 1999 Job time : 14 secs.

Page 1

09/312/77 Page 1 8035. Claims 82-84

Mohamed, A.

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·	(TM)
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 4.70 Seconds 140.296 Million cell updates/sec Mon Oct 4 15:28:18 1999; not generated Run on:

ular output

48

Claim

>MOHAM-312-CLAIM84.PEP (1-31) from moham312177.pep 220 Title: Description: Perfect Score:

1 dlskqmeeeavrlfiewlknggpssgappps 31 sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
l:part1 2:part2 10:part10 11:part11 12:part12 13:part13 10:part14 15:part15 16:part15 17:part17 18:part18 19:part18 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part29 31:part31 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38 39:part39

Mean 24.023; Variance 96.248; scale 0.250 Statistics:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	d. No.	10e-12	1.10e-12	10e-12	10e-12	10e-12	10e-12	.10e-12	1.10e-12	1.12e-10	.22e-08	.4/e-0/	.47e-07	.15e-05	.15e-06	90-00	4.2e-06
	Pred.	1.1		7	7.	7:		7.7		ω 	4	4.	7	7 1	7	7	λ 4.
	Description	Heloderma suspectum e	Exendin-3, for use in	Exendin-4, for use in	Gila monster exendin-	Heloderma horridum ex	Heloderma suspectum e	Gila monster exendin-	Heloderma suspectum p	Leu(14), Phe(25)-exen	Heloderma suspectum e	Exendin-4 (1-30) for	Heloderma suspectum e		H. horridum exendin-3	H. horridum exendin-4	H. horridum exendin-4
	a	R80547	W61769	W61770	W47608	R80545	R80546	W47609	W70288	W61773	R80543	W61771	R80544	W39368	W39301	W39302	W39309
	DB	14.	39	39	30	14	14	30	35	5	14	39	14	5	29	5	59
	Query Match Length	31	30	36	39	39	39	66	87	. 0	31	30	31	30	30	30	30
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	000	0 00	78.6	75.0	75.0	71.8	71.8	71.8	69.5
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28e-0	15e-	.15e-	.26e-	.26e-	"	. 26e-	.26e-	.26e-	. 26e-	. 26e-	.26e-	. 26e-	. 26e-	.26e-	-26e-	, ,	9 6	307.	. 70e	7.0e	7.00	. 26e	206	. 26e	. 2be	. 26e	. 26e	260	9 6	ש
(1-28) amid 5.	.3		۳,	ų.	4-	-3	۳	-4		٠.	n-3	۳,	exendin-4	exendin-3	S-diposo	CHICAN	exendin-4	exendin-3	exendin-4	exendin-4	exendin-4	exendin-4	exendin-3	exendin-4	exendin-3	exendin-3	oxondin-3	exemption of	exenden	exending
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39 W617	29 W393	50FW 00	20 8393	00 M303	29 W393	20 8393	20 8393	605W 00	000	20 8303	000	00	1000	100 M	CM 67	29 W39	29 W39	29 W394	29 W39	29 W393	20 14203	2001	29 W393	29 W393	29 W393	29 W393				
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ALIGNMENTS

Eng J; Why: 95-262627/34. Stimulating/inhibiting insulin release with exendin polypeptide(s) Stimulating/inhibiting insulinus and preventing hyperglycaemia. for treating diabetes mellitus and preventing hyperglycaemia. Claim 7; Columns 13-14; 17pp; English. R80547 is the Heloderma suspectum exendin-4 residues 9-39. It is an insulinotropic peptide activity inhibitor. R80547;
27-FBB-1996 (first entry)
Heloderma suspectum exendin-4 residues 9-39 (Extendin-4(9-39)).
Exendin-4; residues 9-39; Exendin-4(9-39);
Insulnotropic peptides; inhibitor.
Heloderma suspectum. T 1 R80547 standard; peptide; 31 AA. 24-MAY-1993; 066480. 24-MAY-1993; US-066480. (ENGJ/) ENG J. Sequence RESULT

Gaps ö Query Match 100.0%; Score 220; DB 14; Length 31; Best Local Similarity 100.0%; Pred. No. 1.10e-12; Matches 31; Conservative 0; Mismatches 0; Indels

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Exendin-3, for use in treating disorders related to food intake. Exendin-3, for use in treating disorders; cardiac disease; Exendin; obesity; type II diabetes; eating disorders; cardiac disease; insulin resistance syndrome; elevated plasma glucose level; agonist. Heloderma horridum.
W09830231-A1. W61769 standard; peptide; 39 AA. W61769; 29-MAR-1999 (first entry) POST SE PAR

RESULT

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Reducing food intake by administering exendins or their analogues - for treatment of e.g. obesity, type II diabetes, analogues - for treatment of e.g. obesity, type II diabetes, cating disorders and insulin resistance of the invention relates to a new method for treating disorders that are alleviated by reducing food intake, in particular obesity, type II diabetes, eating disorders, insulin resistance syndrome, elevated plasma glucose levels, or the risk of cardiac disease. The method comprises administering an exendin or an exendin agonist. The treatment comprises administering an exendin or cholecystokinin but has a much longer-lasting action (still effective after 6 hours in a mouse model). The present sequence is that of exendin-4 which is one of the preferred compounds for use in the method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                        analogues - for treatment of e.g. obesity, type II diabetes, analogues - for treatment of e.g. obesity, type II diabetes, claims 16, 24; Page 8; 214pp; English.

Claims 16, 24; Page 8; 214pp; English.

The invention relates to a new method for treating disorders that are alleviated by reducing food intake, in particular obesity, type II diabetes, eating disorders, insulin resistance syndrome, elevated plasma glucose levels, or the risk of cardiac disease. The method comprises administering an exendin or an exendin agonist. The treatment reduces appetite and lowers plasma lipid levels. It inhibits food consumption as effectively as amylin or cholecystokinin but has a much longer-lasting action (still effective after 6 hours in a mouse model). The present sequence is that of exendin-3 which is one of the preferred sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-1999 (first entry)
29-MAR-1999 (first entry)
Exendin-4, for use in treating disorders related to food intake.
Exendin, obesity; type II diabetes; eating disorders; cardiac disease; insulin resistance syndrome; elevated plasma glucose level; agonist.
Heloderma suspectum.
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Pred. No. 1.10e-12;
0; Mismatches 0; Indels
                                                                                                                                                                                             Reducing food intake by administering exendins or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 dlskqmeeeavrlfiewlknggpssgappps 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 dlskgmeeeavrlfiewlknggpssgappps 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beeley NRA, Bhavsar S, Prickett KS;
WPI; 98-398796/34.
                                                                                                                                                  Beeley NRA, Bhavsar S, Prickett KS;
WPI; 98-398796/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W61770 standard; peptide; 39 AA.
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Local Similarity 100.0%;
les 31; Conservative
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16-JUL-1998.
07-JAN-1997; US-066029.
07-JAN-1997; US-034905.
08-AUG-1997; US-055404.
14-NOV-1997; US-055404.
(AMYL-) AMYLIN PHARM INC.
                                      14-NOV-1997; US-066029.
07-JAN-1997; US-034905.
08-AUG-1997; US-055404.
14-NOV-1997; US-065442.
(AMYL-) AMYLIN PHARM INC.
16-JUL-1998.
07-JAN-1998; U00449.
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Best Local S
Matches 3
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R80545;
27-FEB-1996 (first entry)
Heloderma horridum exendin-3.
Exendin-3; diabetes mellitus; hyperglycaemia; insulinotropic peptide.
Heloderma horridum.
                                                                                                                                                                                                                                                                                                                                                                                                 Regulating gastrointestinal motility using exendins or their agonists for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations claims 20 and 21; Fig 1; 70pp; English.
W47549 describes a generic exendin agonist, provided that it does have the formula of either exendin-3 (W47608) or exendin-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stimulating/inhibiting insulin release with exendin polypeptide(s) for treating diabetes mellitus and preventing hyperglycaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exendin agonists, which reduce gastric motility and delay gastric emptying, can be used to treat spasm (where associated with acute diverticulties or disorders of the biliary tract or sphincter of oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. They can also be administered to subjects undergoing gastrointestinal diagnostic
                                                                                                                                  Gila monster exendin-3.

Exendin agonist; gastric motility; gastric emptying; treatment; spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity; Gila monster venom; exendin-3.

Heloderma horridum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exendins, components of Gila monster venom, have some sequence similarity to glucagon-like peptides (GLP). They are GLP agenists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.

Sequence 39 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Investigation, particularly radiological or by magnetic resonance
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Pred. No. 1.10e-12;
                                                                                                                                                                                                                                                                                                                                                 (AMYL-) AMYLIN PHARM INC.
Beeley NRA, Gedulin B, Prickett KS, Young AA;
WPI; 98-145351/13.
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Location/Qualifiers
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R80545 standard; peptide; 39 AA.
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                                                                                standard; peptide; 39
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Similarity 100.08;
31; Conservative
                                                                                                                  (first entry)
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24-MAY-1993; US-066480.
(ENGJ/) ENG J.
                                                                                                                                                                                                                                                                                                                                     08-AUG-1996; US-694954.
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                                                                                                                  03-JUL-1998
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N-PSDB; V33163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treating diabetes mellitus and preventing hyperglycaemia. Claim 6; Columns 13-14; 17pp; English.
RR0546 is Heloderma suspectum exacdin-4. It is an insulinotropic peptide, and can therefore be used in the treatment of diabetes mellitus (types I or II), and for the prevention of hyperglycaemia. It normalises hyperglycaemia through glucose-dependent and insulin-(in)dependent mechanisms.
Claim 5; Columns 13-14; 17pp; English. R. 880545 is Heloderma horridum exendin.3. It is an insulinotropic peptide, and can therefore be used in the treatment of diabetes mellitus (types I or II), and for the prevention of hyperglycaemia. It normalises hyperglycaemia through glucose-dependent and insulin-(in)dependent mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FBB-1996 (first entry)
Heloderma suspectum exendin-4.
Exendin-4; diabetes mellitus; hyperglycaemia; insulinotropic peptide.
Heloderma suspectum.
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                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPĪ; 95-262627/34.
Stimulating/inhibiting insulin release with exendin polypeptide(s)
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Pred. No. 1.10e-12;
0; Mismatches 0; Indels
                                                                                                                                                                                Score 220; DB 14; Length 39;
Pred. No. 1.10e-12;
                                                                                                                                                                                                                            0; Indels
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Beeley NRA, Gedulin B, Prickett KS, Young AA;
WPI; 98-145351/13.
                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     JT 6
R80546 standard; peptide; 39 AA.
R80546;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 100.0%;
Local Similarity 100.0%;
nes 31; Conservative
                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUL-1998 (first entry) Gila monster exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-AUG-1996; US-694954.
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24-MAY-1993; 066480.
24-MAY-1993; US-066480.
(ENGJ/) ENG J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heloderma suspectum
                                                                                                                                        39 AA;
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Modified_site
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Matches
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ID R8
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06-NOV-1998 (first entry)
Heloderma suspectum proexendin peptide.
Heloderma suspectum proexendin; exendin N-terminal peptide; ENTP;
exendin 4 peptide; exendin 3 gene; Heloderma horridum; metabolic disease;
drug screening; endocrine tunur; organ failure; cell metabolism;
diabetes; reptilian venom peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Heloderma suspectum proexendin peptide is encoded by its CDNA which was isolated from a H. suspectum salivary gland cDNA library. The proexendin protein comprises of a novel exendin N-terminal peptide (EMTP) linked to the N-terminal of the exendin 4 peptide by a consensus dipeptidyl peptidase cleavage site. The proexendin companies to clone or identify related sequences (e.g. the exendin 3 gene of Heloderma horridum, mutant alleles and proexendin gene regulatory defects associated with metabolic disease) and species the proexendin peptide can be used to raise antibodies. Anti-proexendin antibodies are claimed to be useful for diagnosing conditions associated
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                                                                                                                                                                             diverticulitis or disorders of the biliary tract or sphincter of diverticulitis or disorders of the biliary tract or sphincter of oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. They can also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic resonance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding proexendin - used to diagnose and treat, e.g. endocrine tumours, also to treat poisoning by reptile venom Claim 3; Fig 2; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exendins, components of Gila monster venom, have some sequence similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US$424286) for treatment of diabetes and prevention of hyperglycaemia.
                                                      provided that it does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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/note= "Dipeptidyl peptidase cleavage site"
Claims 20 and 21; Fig 1; 70pp; English.
W47549 describes a generic exendin agonist, provided that i
have the formula of either exendin-3 (W47608) or exendin-4
(W47609).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 39;
                                                                                                                                                    Exendin agonists, which reduce gastric motility and delay
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Pred. No. 1.10e-12;
0; Mismatches 0;
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/note= "Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .r 8
W70288 standard; Protein; 87 AA.
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Drucker DJ;
WPI; 98-447230/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
Local Similarity 100.0%;
hes 31; Conservative
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07-FEB-1997; GB-002582.
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/note=
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/note=
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MOHAM-312-CLAIM84.PEP.rag

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Reducing food intake by administering exendins or their analogues - for treatment of e.g. obesity, type II diabetes, eating disorders and insulin resistance caring disorders and insulin resistance caring disorders and insulin resistance caring disorders to a new method for treating disorders that are alleviated by reducing food intake, in particular obesity, type II diabetes, eating disorders, insulin resistance syndrome, elevated plasma glucose levels, or the risk of cardiac disease. The method comprises administering an exendin aponist. The treatment reduces appetite and lowers plasma lipid levels. It inhibits food consumption as effectively as amylin or cholecystokinin but has a much longer-lasting action (still effective after 6 hours in a mouse model). The present sequence is that of an exendin-4 variant which is one of
failure), for identifying other regulators of cell metabolism, in drug screens and for treating metabolic diseases (e.g. diabetes) and for neutralising, or detecting, reptilian venom peptides. Sequence 87 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leu(14), Phe(25)-exendin-4 amide, for reducing food intake.
Exendin; obesity, type II diabetes; eating disorders; cardiac disease;
insulin resistance syndrome; elevated plasma glucose level; agonist.
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Heloderma suspectum exendin-4 residues 1-31 (Exendin-4(1-31)).
Exendin-4; residues 1-31; Exendin-4(1-31); diabetes mellitus;
                                                                                                                                    Score 220; DB 35; Length 8/;
Pred. No. 1.10e-12;
....matches 0; Indels
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                                                                                                                                                                                                                                                                                                  56 dlskqmeeeavrlfiewlknggpssgappps 86
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Heloderma suspectum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
39
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Beeley NRA, Bhavsar S, Prickett XS;
WPI; 98-398796/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /i 9
W61773 standard; peptide; 39 AA.
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                                                                                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 31; Conservative
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10-JON-1998; U00449.

14-NOV-1997; US-066029.

07-JAN-1997; US-034905.

08-AUG-1997; US-055404.

14-NOV-1997; US-065442.
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24-MAY-1993; 066480.
24-MAY-1993; US-066480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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ID R8
DC R8
DD 27
DE H6
KW EX
KW hy
OS H6
PN US
PP 15
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Reducing food intake by administering exendins or their analogues - for treatment of e.g. obesity, type II diabetes, analogues - for treatment of e.g. obesity, type II diabetes, analogues - for treatment of e.g. obesity, type II diabetes, and insulin resistance

The invention relates to a new method for treating disorders that are alleviated by reducing food intake, in particular obesity, type II diabetes, eathing disorders, insulin resistance syndrome, elevated II diabetes, eathing disorders, insulin resistance syndrome, elevated Comprises administering an exendin or an exendin agonist. The method comprises appetite and lowers plasma lipid levels. It inhibits food comprises appetite and lowers plasma lipid levels. It inhibits food consumption as effectively as amylin or cholesystokinin but has a much longer-lasting action (still effective after 6 hours in a mouse model). The present sequence is that of exendin-4 (1-30) or its amide which is common and the preferred compounds for use in the method.
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                                                         WPI: 95-262627/34.

Stimulating/inhibiting insulin release with exendin polypeptide(s) -
Stimulating/inhibiting insulin release with exendin polypeptide(s) -
for treating diabetes mellitus and preventing hyperglycaemia.

Claim 1: Columns 13-14; 17pp; English.

R80543 is the Heloderma suspectum exendin-4 residues 1-31. It is an
insulinotropic peptide, and can therefore be used in the treatment of
diabetes mellitus (types I or II), and for the prevention of
hyperglycaemia. It normalises hyperglycaemia through glucose-dependent
and insulin-(in)dependent mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exendin-4 (1-30) for use in treating disorders related to food intake. Exendin; obesity; type II diabetes; eating disorders; cardiac disease; insulin resistance syndrome; elevated plasma glucose level; agonist.
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Pred. No. 4.22e-08;
0; Mismatches 0; Indels
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27-FEB-1996 (first entry)
Heloderma suspectum exendin-4 residues 1-31-Tyr31
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Beeley NRA, Bhavsar S, Prickett KS;
WPI; 98-398796/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W61771 standard; peptide; 30 AA.
W61771;
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Best Local Similarity 100.0%;
Matches 23; Conservative
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14-NOV-1997; US-065442.
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07-JAN-1997; US-034905.
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07-JAN-1998; U00449.
ENGJ/) ENG J.
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Goeke B. Goeke R. Hoffmann E;
Truncated versions of exendin peptide(s) for treating diabetes -
Increase secretion and biosynthesis of insulin, but reduce those of
Increase secretion and biosynthesis of insulin, but reduce those of
Jucagon, and do not induce hypoglycaemia
Claim 2; Page 27: 150pp; English.

CR peptides w39303-W39420 are fragments of exendin-3 and exendin-4
CC peptides w39303-W39420 are fragments of diabetes melitus. These peptides can stimulate
CC for the treatment of diabetes mellitus, These peptides can stimulate
CC for the treatment of insulin, but have the opposite effect on
Glucagon, and independent of this activity can increase peripheral
CC glucose utilisation. Exendin-3 and exemplin-4 are only active When blood
CS sugar levels are high, so they will not induce hypoglycaemia. Compared
CC with glucagon-like peptide 1 (GLP1) and the known exendins, they are more
CC active (effective at lower doses), more stable to degradation and
CM metabolism and have a longer lasting effect. Truncated forms of this
CC peptide can be made more economically than full length versions.
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Stimulating/inhibiting insulin release with exendin polypeptide(s) -
Stimulating/inhibiting insulin release with exendin polypeptide(s) -
for treating diabetes mellitus and preventing hyperglycaemia.

Claim 2; Columns 13-14; 17pp; English.

R80544 is the Heloderma suspectum exendin-4 residues 1-31, where
the native Pro31 has been replaced with a Tyr residue. It is an
insulinotropic peptide, and can therefore be used in the treatment of
diabetes mellitus (types I or II), and for the prevention of
hyperglycaemia. It normalises hyperglycaemia through glucose-dependent
and insulin-(in)dependent mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-1998 (first entry)
H. horridum exendin-3 peptide derivative #11.
H. scredin-3; exendin-4; diabetes; insulin; secretion; biosynthesis; glucagon reduction; hypoglycaemia; glucose; treatment.
Heloderma horridum.
Exendin-4; residues 1-31; Y-31-Exendin-4(1-31); diabetes mellitus;
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Pred. No. 2.47e-07;
0; Mismatches 0; Indels
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Pred. No. 1.15e-06;
                      hyperglycaemia; Tyr31; insulinotropic peptide Heloderma suspectum.
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Nay 1868 standard; peptide; 30 AA. AG. W39568 standard; peptide; 30 AA. AG. W39568 standard; peptide; 30 AA. DT 05-UNN-1998 (first entry)

DE H. horridum exendin 3 peptide derifter with a glucagon reduction; hypodyycaemia; Nay glucagon reduction; hypodyycaemia; PH Key Loderma horridum. Location/Qualifier FT Modified_site 30

PM Nodified_site 30

PM Nodified_site Antrope "C-terminal PD 11-DEC-1997.

PP 05-UNN-1997; EC2930.

PR 13-SEP-1996; DE-037230.

PR (BOEF) BOEHRINGER MANNHEIM GMBH.

FI GOEKE ) BOEHRINGER MANNHEIM GMBH.

PI GOEKE W. GOEKE M. HOffmann E;

WPI; 98-04219/04.

Truncated versions of exendin pept
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Best Local Similarity 100.0%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          luery Match
Jest Local Similarity 100.0%;
Matches 22; Conservative
                                                                                                      13-JUN-1995.
24-MAY-1993; 066480.
24-MAY-1993; US-066480.
(ENGJ/) ENG J.
Eng J;
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wri; su-ually/ua.

Truncated versions of exendin peptide(s) for treating diabetes -
Increase secretion and blosynthesis of insulin, but reduce those of
increase secretion and blosynthesis of insulin, but reduce those of
glucagon, and do not induce hypoglycaemia

Claim 1; Page 3; 150pp; English.

This peptide is a fragment of exendin-3 isolated from Heloderma

Chorridum. This peptide and its salts, esters and derivatives can be
used to treat diabetes mellitus. They stimulate blosynthesis and
secretion of insulin, but have the opposite effect on glucagon, and
independent of this activity can increase peripheral glucose utilisation.

Exendin-3 and exendin-4 are only active when blood sugar levels are
high, so they will not induce hypoglycaemia. Compared with glucagon-like
peptide 1 (GIP) and the known exendins, they are more active (effective
at lower doses), more stable to degradation and metabolism and have a
longer lasting effect. Truncated forms of this peptide can be made more
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This peptide is a fragment of exendin-4 isolated from Heloderma
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M39302 standard; peptide; 30 AA.
M39302;
US-JUN-1998 (first entry)
H. horridum exendin-4 peptide.
Exendin-3; exendin 4; dlabetes; insulin; secretion; blosynthesis; glucagon reduction; hypoglycaemia; glucose; treatment.
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                                                                                                  05-JUN-1998 (first entry)
H. horridum exendin-3 peptide.
H. saxodin-3; exendin-4; diabetes; insulin; secretion; biosynthesis; glucagon reduction; hypoglycaemia; glucose; treatment.
Heloderma horridum.
                                                                                                                                                                                                                                                                                                                                           /note= "This residue can be any amino acid except Gly"
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05-10N-1997; E02230.
13-SEP-1996; DE-037220.
05-JUN-1996; DE-022502.
(BOEF ) BOEBRINGER MANNHELM GMBH.
GGOEKE B, GOEKE R, HOFFMANN E7,
WPI; 98-042119/04.
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RESULT 14

ID W33301 standard; peptide; 30 AA. AC. W39301; DT 05-U0N-1998 (first entry)
DE H. horridum exendin-3 peptide.

WW Exendin-3; exendin-3 peptide.

WW Glucagon reduction; hypoglycaemia; per of the carton/Qualifler.

ET Modified_site 30

FT Modified_site 30

FT Modified_site 30

FT MOST46584-AI.

PD 11-DEC-1997.

PR 05-UUN-1996; DE-025502.

PR 05-UUN-1996; DE-027520.

CC-100-1996; DE-027720.

CC-100-1996; DE-0
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05-JUN-1996; DE-022502.
(BOEF ) BOEHRINGER MANNHEIM GMBH.
GOEKE B, GOEKE R, HOFFMANN E;
WPI; 98-042119/04.
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Matches 21; Conservative
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horridum. This peptide and its salts, esters and derivatives can be used to trast diabetes mellitus. They stimulate blosynthesis and secretion of insulin, but have the opposite effect on glucagon, and independent of this activity can increase peripheral glucose utilisation. Exendin-3 and exendin-4 are only active when blood sugar levels are high, so they will not induce hygoglycamia. Compared with glucagon-like peptide 1 (GLP1) and the known exendins, they are more active (effective at lower doses) more stable to degradation and metabolism and have a economically than full length versions.
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ö Gaps ó; Query Match 71.8%; Score 158; DB 29; Length 30; Best Local Similarity 100.0%; Pred. No. 1.15e-06; Matches 21; Conservative 0; Mismatches 0; Indels

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Search completed: Mon Oct 4 15:28:38 1999 Job time : 20 secs.

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protein - protein database search, using Smith-Waterman algorithm Mon Oct 4 15:27:49 1999; MasPar time 4.29 Seconds 289.449 Million cell updates/sec MPsrch_pp Run on:

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>MOHAM-312-CLAIM84.PEP (1-31) from moham312177.pep 210-31 1 dlskqmeeeavrlfiewlknggpssgappps 31 Lifte: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

122810 seqs, 40068593 residues

Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Mean 33.166; Variance 59.781; scale 0.555 Atistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	2.54e-27	2.54e-27	8.43e-03	2.53e-02	2.53e-02	5.20e-02	5.20e-02	2.14e-01	4.29e-01	4.29e-01	1.19e+00	1.19e+00	1.19e+00	1.19e+00	1.19e+00	1.67e+00	1.67e+00	1.67e+00	2.32e+00	2.32e+00	2.32e+00	2.32e+00	3.23e+00
	Description	exendin-4 - Gila mons	exendin-3 - Mexican b	qlucagon G2 - North A	genome polyprotein -	genome polyprotein -	glucagon G1 - North A	replicase - phage PP7	glucagon precursor -	glucagon-like peptide	glucagon precursor -	glucagon-like peptide	glucagon-like peptide	glucagon - chinook sa	glucagon I precursor	glucagon II precursor	glucagon precursor -	probable transcriptio	acetyl-CoA carboxylas	probable acylphosphat	glucagon 2 precursor	methylated-DNAprote	ybdN protein - Escher	glucagon precursor -
SUMMARIES	ID	HWGH4G	HWGH3Z	S44472	ZLVNSB	ZLVNPV	S44471	S46978	GCIDC	S44473	GCFGB	B61125	C61125	151093	I51058	151057	GCGXA	E71023	260200	G64837	GCAF2	XUHUMC	H64793	CCONC
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,	* Query Match	100.0	100.0	41.4	40.0	40.0	39.1	39.1	37.3	36.4	36.4	35.0	35.0	35.0	35.0	35.0	34.5	34.5	34.5	34.1	34.1	34.1	34.1	33.6
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33.2 300 2 S34116 transcription factor 4.48e+00 33.2 402 1 RSBP18 probable integrase - 4.48e+00 33.2 1212 2 S27771 RNA-directed DNA poly 4.48e+00 33.2 1272 2 S27771 RNA-directed DNA poly 4.48e+00 33.2 1352 2 G71051 probable APP-dependen 4.48e+00 probable APP-dependen 4.48e+00 probable APP-dependen 4.48e+00 hypothetical protein 4.48e+00 hypothetical protein 6.20e+00 48678 protein 4.70e+00 48678 protein 4.70e+00 8.54e+00	ALIGNMENTS	HWGH4G #type complete exendin-4 - Gila monster #formal_name Heloderma suspectum #common_name Gila monster 31.Mar-1993 #sequence_revision 31-Mar-1993 #text_change		E 1/2 H	<pre>cells. by #superfamily glucagon amidated carboxyl end; duplication; venom #modified_site amidated carboxyl end (Ser) #status experimental *length 39 #molecular-weight 4188 *checksum 9570</pre>	100.0%; Score Similarity 100.0%; Pred. 31; Conservative 0; M	DLSKQMEEBAVRLFIEWLKNGGPSSGAPPPS 39 	HWGH3Z #type complete exendin-3 - Mexican beaded lizard #formal_name Heloderma horridum #common_name Mexican beaded 11_laard 31_laard 31_Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997 A23674 A23674 Eng, J.; Andrews, P.C.; Kleinman, W.A.; Singh, L.; Raufman, J.P.
7 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		RESULT 1 ENTRY TITLE ORGANISM DATE	ACCESSIONS REFERENCE #authors #journal #title	#cross-re: #accession ##mole: ##resic	CEASSIFICATION KEYWORDS FEATURE 39 SUMMARY	Query Match Best Local S Matches	13 - 1 5	RESULT 2 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors

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Biochem. J. (1994) 300:339-345
Characterization of insulins and proglucagon-derived peptides
from a phylogenetically ancient fish, the paddlefish
(Polyodon spathula).
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1-31 ##!abel NGU
the sequence from Fig. 3 is inconsistent with that from
Fig. 5 in having 29-Glu
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                                                                                 #journal J. Biol. Chem. (1990) 265:20259-20262
#title Purification and structure of exendin-3, a new pancreatic
secretagogue isolated from Heloderma horridum venom.
#cross-references MuID:91056067
#accession A23674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conzelmann, K.K.; Cox, J.H.; Schneider, L.G.; Thiel, H.J. Virology (1990) 175:485-499
Molecular cloning and complete nucleotide sequence of the
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30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change
29-May-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #superfamily glucagon
carbohydrate metabolism; duplication; hormone; pancreas
                                                                                                                                                                                                 #modified_site amidated carboxyl end (Ser) #status
                                                                                                                                                                                                                                #molecular-weight 4204 #checksum 9591
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#length 31 #molecular-weight 3682 #checksum 7826
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Pred. No. 8.43e-03;
...amatches 5; Indels
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Pred. No. 2.54e-27;
0; Mismatches 0; Indels
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RNA-directed RNA polymerase (EC 2.7.7.48)
                                                                                                                                                                                                                                                                                                                 9 DLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS 39
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Best Local Similarity 100.0%;
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Similarity 57.1%;
12; Conservative
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S44472
                                                                  ##molecule_type protein
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##residues 1-31 ##;
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Best Local Similarity
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Tordo, N.; Poch, O.; Ermine, A.; Keith, G.; Rougaon, F. Virology (1988) 165:555-576
Completion of the rabies virus genome sequence determination:
highly conserved domains among the L (polymerase) proteins
of unsegmented negative-strand RNA viruses.
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#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:3914-3918
#title Walking along the rables genome: is the large G-L intergenic region a remnant gene?
#cross-references MUID:86233343
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RNA-directed RNA polymerase (EC 2.7.7.48)
#formal_name rables virus
30-Sep-1999 #sequence_revision 30-Sep-1989 #text_change
29-May-1998
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#domain transmembrane #status predicted #label TM2
#length 2127 #molecular-weight 242977 #checksum 9107
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nucleotidyltransferase; RNA binding; RNA biosynthesis;
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nucleotidyltransferase; RNA binding; RNA biosynthesis;
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Pred. No. 2.53e-02;
6; Mismatches 6; Indels
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genome polyprotein - rabies virus (strain PV)
                                                                                                                                    ##cross-references GB:M31046; NID:g333556; PID:g333561
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attenuated rabies virus SAD B19.
#cross-references MUID:90223994
#accession E34746
                                                                            ##molecule_type genomic RNA
##residues 1-2127 ##label CON
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##residues 1-28 ##label TO2
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Local Similarity 42.9%;
nes 9; Conservative
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Best Local Similarity 42.9%;
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#formal_name Ictalurus punctatus #common_name channel catfish
31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
                                                                                                                                                    Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.
Biochem. J. (1994) 8100:339-345
Characterization of insulins and proglucagon-derived peptides
from a phylogenetically ancient fish, the paddlefish
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9444/1  #type complete
glucagon Gl - North American paddlefish (Polyodon spathula)
#formal_name Polyodon spathula
18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change
20-Mar-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S46978 #type complete replicase - phage PP7 #formal_name phage PP7 | 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997 |
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Nucleotide sequence of a single-stranded RNB phage from
Pseudomonas aeruginosa; Kinship to coliphages and
conservation of regulatory RNA structures.
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##experimental_source panoreas
FFICATION #superfamily glucadon
OS carbohydrate metabolism; duplication; hormone; panoreas
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J. Biol. Chem. (1985) 260:3910-3914
Isolation and structures of glucagon and glucagon-like
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#fresidues 1-552 ##label OLS
##cross-references EMBL:X80191; NID:9517241
# #cross-references #molecular-weight 63300 #checksum 8424
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#length 31 #molecular-weight 3751 #checksum 7808
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Pred. No. 5.20e-02;
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3; Mismatches 6; Indels
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Matches 9; Conservative
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Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.
Blochem. J. (1994) 300:339-345
Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish
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glucagon; glucagon-36 (oxyntomodulin); glucagon-like peptide
1; glucagon-like peptide 2
#formal_name Rana catesbeiana #common_name bullfrog
31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
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#product glucagon-like peptide 1 #status experimental
#label GL1
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J. Biol. (1988) 263:9746-9751
Isolation of peptide hormones from the pancreas of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #formal_name Polyodon spathula
18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change
20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                      #superfamily glucagon
carbohydrate metabolism; duplication; hormone; pancreas
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                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                            Score 82; DB 1; Length 63;
Pred. No. 2.14e-01;
7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 80; DB 2; Length 30;
Pred. No. 4.29e-01;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCFGB *type fragments
glucagon precursor - bullfrog (fragments)
peptide from catfish pancreas.
#cross-references MUID:85157536
#accession A05166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *superfamily glucagon
duplication; hormone; pancreas
                                                                                                                                                                                                                                                                                                                                *length 63 #checksum 9366
                                                                                                                                    ##molecule_type protein
##residues 30-63 ##label AND2
                                                                ##molecule_type_protein
##residues 1-29 ##label AND1
ccession A05167
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##residues 1-30 ##label NGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 DVSSYLQDQAAKDFITWLKSGQP 60
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43.5%;
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:larity 56.3%;
Conservative
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Best Local Similarity
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#journal Gen. Comp. Endocrinol. (1991) 82:23-32

#title The primary structure of glucagon-like peptide but not insulin has been conserved between the American eel, Anguilla rostrata and the European eel, Anguilla anguilla.

#cross-references MUID:91340068
#accession B61125
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#label GL2
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#product glucagon-like peptide 1 #status experimental
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#label GLP\
#modified_site amidated carboxyl end (Arg) #status
predicted
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glucagon-like peptide - American eel
#formal name Anguilla rostrata *common_name American eel
10-Mar-1994 *sequence_revision 10-Mar-1994 *text_change
                                                                                                                                                                                       Jobania
##molecule_type protein
##residues 69-101 ##label PO3
IFICATION #superfamily glucagon
RDS carbohydrate metabolism; duplication; hormone; pancreas
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bullfrog (Rana catesbeiana). Amino acid sequences of pancreatic polypeptide, oxyntomodulin, and two glucagon-like peptides.
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                                                                                                                                                                                                                                                                                      *product glucagon-36 (oxyntomodulin) *status experimental *label G36\
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80; DB 1; Length 101; Pred. No. 4.29e-01; 6; Mismatches 7; Indels
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amidated carboxyl end; duplication
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                                                                                                                                        ##molecule_type protein
##residues 37-68 ##label POL
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##residues 1-30 ##label CON
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                                                                                      ##molecule_type protein
##residues 1-36 ##label PO2
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Best Local Similarity 43.5%;
Matches 10; Conservative
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B61125
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37-67
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RESULT ENTRY

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                                          #authors Conlon, J.M.; Andrews, P.C.; Thim, L.; Moon, T.W.
#journal Gen. Comp. Endocrinol. (1991) 82:23-32
#title The primary structure of glucagon-like peptide but not insulin has been conserved between the American eel, Anguilla rostrata and the European eel, Anguilla anguilla.
#cross-references MIDE:91340068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glucagon I precursor - rainbow trout #formal_name Oncorhynchus mykiss #common_name rainbow trout 13.Sep-1996 #sequence_revision 13-Sep-1996 #text_change
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#sequence_revision 10-Mar-1994 #text_change
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#title Trout and chicken proglucagon: alternative splicing mrNA transcripts encoding glucagon-like peptide 2.
                                                                                                                                                                                                                                                                                                                                                experimental **length 30 **molecular-weight 3376 **checksum 6092
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151058; 151299; 151056; 151037; 151036; 151300
A55895
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                                                                                                                                                                                        Irwin, D.M.; Wong, J.
Mol. Endocrinol. (1995) 9:267-277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##cross-references EMBL:019920; NID:g7
CLASSIFICATION #*superfamily glucagon
duplication #tergeth SG #checksum 1440
#length 66 #checksum 1440
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##molecule_type mRNA
***residues 1-66 ##label IRW
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Best Local Similarity 38.1%;
Matches 8; Conservative
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           21-Nov-1997
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#authors
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ORGANISM
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#authors Irwin, D.M.; Wong, J.
#journal Mol. Endocrinol. (1995) 9:267-277
#title Trout and chicken proglucagon: alternative splicing generates
#cross-references MUID:95295739
#cross-references MUID:95295739
#accession IS1057
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#formal_name Oncorhynchus mykiss #common_name rainbow trout
13.5ep-1996 #sequence_revision 13.5ep-1996 #text_change
21-Nov-1997
IS1059; IS1039; IS1038
                                                                                                                                                      ##residues
##cross-references EMBL:U19917; NID:9736364; PID:9736365; GB:S78475;
##cross-references NID:9999384; PID:999385
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#length 178 #molecular-weight 20034 #checksum 5250
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##molecule_type DNA
##residues 113-123 ##label IR3
                                                                                                                                                                                                                                                                                                                                                                                                         ##status
##molecule_type DN
##molecule_type DN
##residues
##coss-references EMBL:U19919; NID:g736374; PID:g736377
##stest:...
                                                                                                                                                                                                                           ##status preliminary; translated from GB/EMBL/DDBJ ##status preliminary; translated from GB/EMBL/DDBJ ##moleculetype DMB ## # 113 - 123 # # label IR5 # **cross-references EMBL: U19918; NID: 9736373; PID: 9736376
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##residues 1-178 ##label IRW
##cross-references EMBL:U19914; NID:9736362; PID:9736363
#acrossion 151039
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##cross-references EMBL:U19915; NID:g736368; PID:g736371
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##residues 58-123 ##label IR3
##cross-references EMBL:U19913; NID:g736360; PID:g736361
reession IS1037
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Pred. No. 1.19e+00;
8; Mismatches 5; Indels
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#superfamily glucagon
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Best Local Similarity 38.1%;
Matches 8; Conservative
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##residues 113-
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#introns 123/2
CLASSITGATION # $100000
KEYWORDS
CLASSITGATION # $1000000
KEYWORDS

#length 178 #molecular-weight 19998 #checksum 4464

Query Match
Best Local Similarity 38.1%; Pred. No. 1.19e+00;
Matches 8; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Db 98 DVSTILODQAANDFVSWLKS 118

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Qy 1 dlskqmeeeavrlfiewlkng 21

Search completed: Mon Oct 4 15:28:01 1999
Job time: 12 secs.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Oct 4 15:26:51 1999; MasPar time 3.25 Seconds 269.668 Million cell updates/sec ular output not generated.

Run on:

>MOHAM-312-CLAIM84.PEP (1-31) from moham312177.pep 220 1 dlskqmeeeavrlfiewlknggpssgappps 31 bescription:
 Perfect Score:
 Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues üea⊥cined:

Minimum Match 0% Listing first 45 summaries nort-processing:

Database:

swiss-prot37 1:swissprot

Mean 33.941; Variance 55.026; scale 0.617 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	1.73e-30	1.73e - 30	6.16e-03	6.16e-03	4.33e-02	1.35e-01	4.12e-01	4.12e-01	5.93e-01	8.51e-01	8.51e-01	8.51e-01	8.51e-01	8.51e-01	8.51e-01	-	1.74e+00	1.74e+00	1.74e+00	1.74e+00	1.74e+00	3.50e+00	3.50e+00
	Description	EXENDIN-3.	EXENDIN-4 PRECURSOR.	RNA POLYMERASE BETA SU	RNA POLYMERASE BETA SU	GLUCAGON PRECURSOR (FR	GLUCAGON PRECURSOR (FR	GLUCAGON-LIKE PEPTIDE	GLUCAGON II.	GLUCAGON PRECURSOR (FR	PUTATIVE ACYLPHOSPHATA	GLUCAGON PRECURSOR.	GLUCAGON II PRECURSOR.	METHYLATED-DNAPROTEI	UREA TRANSPORTER, ERYT	HYPOTHETICAL 47.8 KD P	GLUCAGON PRECURSOR (FR	TRANSCRIPTION INITIATI	TRANSCRIPTION INITIATI	CONJUGAL TRANSFER PROT	INTEGRASE.	CITRATE LYASE ALPHA CH	OXIDASE	HYPOTHETICAL PROTEIN M
	ID	ЕХЕЗ_НЕГНО	EXE4_HELSU	RRPL_RABVS	RRPL_RABVP	GLUC_ICTPU	GLUC_RANCA	GLUM_ANGAN	GLU2_ORENI	GLUC_LEPSP	ACYP_ECOLI	GLUC_CARAU	GLU2_LOPAM	MGMT_HUMAN	UT1_HUMAN	YBDN_ECOLI	GLUC_ONCKI	TF2B_PYRWO	TF2B_PYRFU	TRBB_AGRI6	VINT_BPPH8	CILA_ECOLI	COX2_LOCMI	Y124_METJA
	DB	H	-	Н	Н	Н	Н	П	Н	М	Н	Н	-	7	Н	Н	~	Н	Н	Н	Н	Н	Н	Н
	Length	98	87	2127	2142	71	103	30	33	78	92	121	122	207	389	406	99	261	300	323	402	510	227	1075
æ	Query Match	100.0	100.0	40.0	40.0	37.7	36.4	35.0	35.0	34.5	34.1	34.1	34.1	34.1	34.1	34.1	33.6	33.2	33.2	33.2	33.2	33.2	32.3	32.3
	Score	220	220	88	88	83	80	77	77	16	75	75	75	75	75	75	74	73	73	73	73	73	71	71
	Result No.	T	7	m	4	5	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

4.94e+00 6.94e+00 6.94e+00 6.94e+00 6.94e+00 9.73e+00 9.73e+00 9.73e+00 9.73e+00 9.73e+01 1.36e+01 1.36e+01 1.36e+01 1.36e+01 1.36e+01 1.36e+01 1.36e+01 1.36e+01 1.36e+01 1.36e+01 1.36e+01 1.36e+01 1.36e+01 1.36e+01 1.36e+01 1.36e+01	
GLUCAGON PRECURSOR. 4-TYPE SODIUM ATP SYNT ACLD BETA-FRUCTOFURANO ENCINUCLEASE ABC SUBUN GENOME POLYPROTEIN [CO PYRLDOXAMINE 5'-PHOSPH IG MU CHAIN C REGION. ADENOSTLAMOCYSTEINASE ABSCISIC ACID-INSENSIT ACETT-COA CARBOXYLASE ERYTHRONOLIDE SYNTHASE GLUCAGON PRECURSOR. HYPOTHETICAL 55.1 KD P KARYOGHATTALA 78.8 KD P HYPOTHETICAL 78.8 KD P	
TADM BHISN WYADW BHISN WYADW BHISN WYAD BHENT POLG PENYT POLG PENYT POLG PENYT SAHIJANAT ABIJARATH ABIJARATH ABIJARATH COAC_TEAST ERYZ_SACER GLUC_MOUSE GLUC_MOUSE GLUC_MOUSE GLUC_BOUN GLUC_BOUN KACA_BACSU KACA_BACSU KACA_BACSU KACA_BACSU KARA_BACSU KARA_BACSU KARA_BACSU KARA_BACSU KARA_BACSU KARA_BACSU	
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151 30658 30658 30658 20268 2027 20233 3567 1180 1180 1180 1180 1180 1180 1180 118	
88 4 4 4 4 4 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
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ALIGNMENTS

) URIA; SQUAMATA; MA.		MAN JP.; ncreatic		CILVIII. INIERACIS						Length 39; ; Indels 0; Gaps							HPTA. COHAMATA:
39 AA.	UPDATE) N UPDATE)	EXENDIN'3. HELODERMA HORRIDUM HORRIDUM (MEXICAN BEADED LIZARD). EUVEARVOTA, METAZOA, CHORDATA; VERTEBRATA; LEPIDOSAURIA; EGIRPOGIOGEA: ANGITHMAPPHA: HELODERMATIDAE: HELODERMA		SINGH L., RAUFMAN JP.; in-3, a new pancreatic	secretagogue isolated from Heloderma horridum venom."; J. BIOL. CHEM. 265:20259-20262(1990).	FUNCTION: HAS A VIP/SECRETIN-LIKE BIOLOGICAL ACTIVITY WITH THE EXENDIN RECEPTOR.	GON FAMILY.			ino	AB598FD3 CRC32;	DB 1; 1.73e-30; tches 0	39	31		87 AA.	UPDATE)	ANNOTATION UPDATE)	(GILA MONSTER).
PRT;	CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE)	UM (MEXICAN AIA; VERTEB HELODERMA		NMAN W.A., SINGH re of exendin-3,	m Heloderma 20262(1990)	ECRETIN-LIK PTOR.	о тне списа	Ŋ; 1.	 T.	MIDATION.		Score Pred. 0; M	GGPSSGAPPPS	ggpssgappps		PRT;	CREATED) LAST SEQUENCE UPDATE)	T ANNOTATIC	(GILA MONSTER).
STANDARD;	(REL. 17, CREAT (REL. 17, LAST (REL. 22, LAST	RRIDUM HORRID ETAZOA; CHORD • ANGITMORPHA		MEDLINE; 91056067. BNG J., ANDREW P.C., KLEINMAN W.A., "Purification and structure of exen	isolated fro M. 265:20259-	: HAS A VIP/SECKET EXENDIN RECEPTOR.	SIMILARITY: BELONGS TO THE GLUCAGON FAMILY A23674: HWGH3Z.	PROSITE; PS00260; GLUCAGON;	PFAM; PF00123; hormone2; I HSSP: P01274: 1GCN	GUCAGON FAMILY; VENOM; AMIDATION.	¥;	100.08; Similarity 100.08; 31; Conservative	DLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS	dlskqmeeeavrlfiewlknggpssgappps		STANDARD;	22, 36,	9 (REL. 36, LAST	SUSPECTUM (GILA
EXE3_HELHO	01-FEB-1991 01-FEB-1991 01-MAY-1992	EXENDIN-3. HELODERMA HO EUKARYOTA; M	[1] SEQUENCE.	MEDLINE; 910 ENG J., ANDR "Purificatio	secretagogue J. BIOL. CHE	-!- FUNCTION: WITH THE	-!- SIMILARITY: BEL PIR: A23674: HWGH3Z	PROSITE; PS0	PFAM; PF0012	GLUCAGON FAM	SEQUENCE 3	Query Match Best Local Simi Matches 31;	9 DLSKOME	1 dlskqme	LT 2	EXE4_HELSU P26349:	01-MAY-1992 15-JUL-1998	15-JUL-1998	
KESOLT TD BI	2222	888	R R R	*	R.	ខូខ	ខ្លួ	DR.	ם מ	ÉŽ:	SO	28.8	Q	δλ	RESULT	a S	占占	TO	S S

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Query Match 40.0%;
Best Local Similarity 42.9%;
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RRPL_RABVP
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                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute of There are no restrictions on its use by non-profit institutions as long as its content is in no way modifised and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
MEDLINE; 90223994.
CONZELMANN K.-K., COX J.H., SCHNEIDER L.G., THIEL H.-J.;
CONZELMANN K.-K., COX J.H., SCHNEIDER L.G., THIEL H.-J.;
"Molecular cloning and complete nucleotide sequence of the attenuated rabies virus SAD B19.";
VIROLOGY 175:485-499(199)
-:- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
-:- SUBUNIT: THOUGHT TO POPEN A TRANSCRIPTION COMPLEX WITH THE NUCLEOCAPSID (N) PROTEIN.
-:- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND
                                                                                                                                      MEDLINE; 92218391.
ENG J., KLEINMAN W.A., SINGH L., SINGH G., RAUFMAN J.-P.;
ENG J., KLEINMAN W.A., SINGH L., SINGH G., RAUFMAN J.-P.;
I'Isolation and characterization of exendin-4, an exendin-4
from Heloderma suspectum venom. Further evidence for an exendin
receptor on dispersed acini from guinea pig pancreas.";
J. BIOL. CHEM. 267:7402-7405(1992).
-!- FUNCTION: HAS A VIP/SECRETIN-LIKE BIOLOGICAL ACTIVITY. INTERACTS
WITH THE EXENDIN RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AGG-1990 (REL. 15, CREATED)
01-AGG-1990 (REL. 15, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
KNA POLYMERASE BETA SUBUNIT (EC 2.7.7.48) (LARGE STRUCTURAL PROTEIN)
(L PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXENDIN-4.
AMIDATION (G-87 PROVIDE AMIDE GROUP).
6C1A8FD5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L.
RABIES VIRUS (STRAIN SAD B19).
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;
RHABDOVIRIDAE; LYSSAVIRUS.
                              SEQUENCE FROM N.A.
CHEN Y.E., DRUCKER D.J.;
SUBMITIED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
SCLEROGLOSSA; ANGUIMORPHA; HELODERMATIDAE; HELODERMA
                                                                                                                                                                                                                                                                           WITH THE EXENDIN RECEPTOR.
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 077613; G1916067; -.
PIR: A42486; HWGH4G.
PROSITE; PSO0260; GLUCAGON; 1.
PFAM: PFO0123; hormone2: 1.
GLUCAGON FAMILY; VENOM; AMIDATION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 DLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 AA; 9479 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARAMYXOVIRUSES
                                                                                       [2]
SEQUENCE OF 48-86.
                                                                                                                           TISSUE-VENOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 3
RRPL_RABVS
P16289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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PROC. NATL. ACAD. SCI. U.S.A. 83:3914-3918(1986).
-!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
-!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 86233343.
TORDO N., POCH O., ERMINE A., KEITH G., ROUGEON F.;
"Walking along the rables genome: is the large G-L intergenic region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1989 (REL. 11, CREATED)
01-JUL-1990 (REL. 13, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
RAP POLYMERASE BETA SUBUNIT (EC 2.7.7.48) (LARGE STRUCTURAL PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TORDO N., POCH O., ERMINE A., KEITH G., ROUGEON F.;
"Completion of the rables virus genome sequence determination: high
conserved domains among the L (polymerase) proteins of unsegmented
negative-strand RNA viruses.";
VIROLOGY 165:565-576(1988).
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-1- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND PARAMYXOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.0%; Score 88; DB 1; Length 2127; Best Local Similarity 42.9%; Pred. No. 6.16e-03; Matches 9; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RUS (STRAIN PASTEUR / PV).
SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Al40/1, CT-10.
PIR; A29248; ZLVNPY.
PIR; E24887; E24887.
FRANSFRASE; RNA-DIRECTED RNA POLYMERASE.
TRANSFRASE; 244485 MW; D8DIEB8F CRC32;
                                                                                                                                                                                                                                                        EMBL; M31046; G333561; -.
PIR; E34746; ZIVNSB.
TRANSFASE; RNA-DIRECTED RNA POLYMERASE.
SEQUENCE 2127 AA; 242977 MW; A4044A1E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 88; DB 1; LA Pred. No. 6.16e-03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 NLNSPLIEDPARLMLEWLKTG 57
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1 dlskgmeeeavrlfiewlkng 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHABDOVIRIDAE; LYSSAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M13215; G333590; -. EMBL; A14671; G492973; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RABIES VIRUS
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1 dlskqmeeeavrlfiewlkng 21
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Matches 10; Conser
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TISSUE-PANCREAS;
                                       SSUE-PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLUM_ANGAN
P41521;
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SEQUENCE
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NON_CONS
PEPTIDE
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PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLUCAGON PRECURSOR (FRAGMENT).
ICTALURUS PUNCTATUS (GRANNEL CAPETSH).
EUKARYOTA, METAZOA; CHORDARA, VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEDOSTEI; BUTELEOSTEI; OSTARIOPHYSI; SILURIFORMES; ICTALURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLUC_RANCA STANDARD; PRT; 103 AA.
P15438; P15439; P15440;
01-APR-1990 (REL. 14, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR (FRACHENTS).
RANA CATESBEIANA (BULL FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; NEGOBATRACHIA; RANOIDEA; RANIDAE; RANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 85157536.
ANDREWS P.C., RONNER P.;
"Isolation and structures of glucagon and glucagon-like peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catfish pancreas.";
J. BICL. CHEM. 260:3910-3914(1985).
-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
THE BLOOD SUGAR LEVEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-!- X'S IN THE SEQUENCES WITH AMERICAN
GOOSEFISH SEQUENCES.
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
PIR; A05166; GCIDC.
PROSITE; PRO0260; GLUCAGON; 2.
PREAM: PF00123; hormone2; 2.
HSSP: P01274; 1GCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
   Indels
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E -> D (IN REF. 2).
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Pred. No. 4.33e-02;
                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1986 (REL. 03, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C49ED93A CRC32;
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   Mismatches
                                                                                                                                                                                                                                                                                                         71 AA
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                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 dlskqmeeeavrlfiewlknggp 23
   9;
                                                                              37 NLNSPLIEDPARLMLEWLKTG 57
                                                                                                                             8173 MW;
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Best Local Similarity 47.8%;
Matches 11; Conservative
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLUCAGON FAMILY; HORMONE.
                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29
71
53
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53
71
71 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 87156787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IISSUE-PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-PANCREAS;
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6
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P04093;
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SEQUENCE
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       Matches
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REE. 32, LAST SEQUENCE UPDATE)
610CAGON-LIKE PEPTIDE (GLP)
ANGUILLA ANGUILLA (EUROPEAN FRESHWATER EEL), AND
ANGUILLA ROSTRATA (AMERICAN EEL).
EUKARYCHA, METAZOA, CHORDARA, VERTEBRATA, ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; ANGUILLIFORMES; ANGUILLIDAE; ANGUILLA.
MEDIJIRE; 88257102.

POLLOCK H.G., HAMILTON J.W., ROUSE J.B., EBNER K.E., RAWITCH A.B.; POLLOCK H.G., HAMILTON J.W., ROUSE J.B., EBNER K.E., RAWITCH A.B.; "Isolation of peptide hormones from the pancreas of the bullfrog (Rana catesbelana). Amino acid sequences of pancreatic polypeptide, oxyntomodulin, and two glucagon-like peptides."; J. BIOL. CHEM. 263:9746-9751(1988).

J. BIOL. CHEM. 263:9746-9751(1988).

THE BLOOD SUGAR LEVEL.

-!- FUNCTION: PROMOTES HYPROLYEIS OF CLICS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

-: X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH OTHER SPECIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 91340068.
CONTON J.W., ANDREWS P.C., THIM L., MOON T.W.;
CONDON J.W., ANDREWS P.C., THIM L., MOON T.W.;
been conserved between the American eel, Anguilla rostrata and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 4.12e-01;
7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 GLUCAGON-LIKE PEPTIDE 2.
11719 MW; D43EDFC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 80; DB 1; Len
Pred. No. 1.35e-01;
6; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buropean eel, Anguilla anguilla.";
3EN. COMP. ENDOCRINOL. 82:23-32(1991).
-!- SIMILARITY: BELONGS TO THE GLOCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27E8C37D CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 DMSSYLEEKAAKEFVDWLIKGRP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; B61125, B61125.
PIR; C61125, C61125.
PROSITE; P800256; GLUCAGON; 1.
PFAM; PFOLO123; hormone2; 1.
HSSP; P01274; 1GCN.
                                                                                                                                                                                                                                                                                                                                                                 PIR, B28091; GCEGB.
PROSITE; PS00260; GLUCAGON; 3.
PFAM; PF00123; hormone2; 3.
HSSP; P01274; 1GCN.
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Best Local Similarity 38.1%;
Matches 8; Conservative
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PEPTIDE
STATEMENT
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                                                         01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
61-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
620CAGON II.
03. OREOCHENDAIS ULLOTICAS (NILE TILAPIA NILOTICA).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI: BUTELEOSTEI; ACANHOPTERYGII; PERCOMORPHA; PERCIFORMES;
LABROIDEI; CICHLIDAE; TILAPIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEPISOSTEUS SPATULA (ALLIGATOR GAR) (ATRACTOSTEUS SPATULA).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
SEMIONOTIFORMES; LEPISOSTEIDAE; LEPISOSTEUS.
                                                                                                                                                                                          MEDLINE, 95384941.

NGUYEN T.M., WRIGHT J.R. JR., NIELSEN P.F., CONLON J.M.;

"Characterization of the pancreatic hormones from the Brockmann body of the tilapia: implications for islet xenograft studies.";

COMP. BIOCHEM. PHYSIOL. 111C:33-44(1995).

-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation and structures of alligator gar (Lepisosteus spatula) insulin and pancratic polypeptide.";
GEN. COMP. ENDOCRINOL. 67:375-382(1987).
-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPLDS, AND RAISES THE BLOOD SUGAR LEYEL.
-!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                      -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation of alligator gar (Lepisosteus spatula) glucagon, oxyntomodulin, and glucagon-like peptide: amino acid sequences of oxyntomodulin and glucagon-like peptide."; especial sequences of GEN. COMP. ENDOCRINOL. 69:133-140(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 88196798.
POLLOCK H.G., KIMMEL J.R., EBNER K.E., HAMILTON J.W., ROUSE J.B.,
LANCE V., RAWITCH A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLLOCK H.G., KIMMEL J.R., HAMILTON J.W., ROUSE J.B., EBNER K.E.
LANCE V., RAWITCH A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                              Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLUC_LEPSP STANDARD; PRT; 78 AA. 209566; 01-MAY-1989 (REL. 10, CREATED) 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE) 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE) GLUCAGON PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                     Score 77; DB 1;
Pred. No. 4.12e-0
                                                                                                                                                                                                                                                                                                                                                                                  3731 MW; DOFD0808 CRC32;
                                     33 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                              PROSITE; PS00260; GLUCAGON; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
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| dlskgmeeeavrlfiewlkng 21
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 38.1%;
                                                                                                                                                                                                                                                                                                                                     PFAM; PF00123; hormone2; 1. HSSP; P01274; 1GCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-36 AND 45-78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 DVSSYLQDQAAKEFVSWLKTG
                                                                                                                                                                                                                                                                                                                                                                   GLUCAGON FAMILY; HORMONE. SEQUENCE 33 AA; 3731 M
                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 88030594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IISSUE-PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-PANCREAS
                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: AN' ACYLPHOSPHATE + H(2)O - A FATTY ACID ANION + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE; 97426617.
BLATINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BUFLAND V.,
RILEY M., COLLADO-VIDES J., GIASMER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESCHERICHIA COLI.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH AMERICAN GOOSEPISH SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAU B., SHAO Y.; "The complete genome sequence of Escherichia coli K-12."; SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                     GLUCAGON-36 (OXYNTOMODULIN). GLUCAGON-LIKE PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 5.93e-01;
7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                         DB 1; Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! - SIMILARITY: HIGH, WITH VERTEBRATE ACYLPHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (REL. 36, LAST SEQUENCE UPDAIE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PUTATIVE ACYLPHOSPHATASE (EC 3.6.1.7) (ACYLPHOSPHATE
                                             -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY. PIR; S06339; GCGXA. PROSITE; PSO0.506; GLUCAGON; 2. PRAME PF00123; hormone2; 2. HSSP; P01274; IGCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 AA; 10300 MW; 599A4C0C CRC32;
                                                                                                                                                                                                                                                                                        509ED9D3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECGGENE; EG13726; YCCX.
PROSITE; PS00150; ACYLPHOSPHATASE_1; 1.
PROSITE; PS00151; ACYLPHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                                           Score 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (REL. 36, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                            53 DVSSYLQDQAAKKFVTWLKQG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 dlskqmeeeavrlfiewlkng 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000199; G1787203; -.
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                                                                                                                                                                                                                                                                                   78 AA; 8990 MW;
                                                                                                                                                                                                                                                                                                                                         34.5%;
38.1%;
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 38.1.,
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                  GLUCAGON FAMILY; HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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P75877;
                                                                                                                                                                                                                                                             PEPTIDE
SEQUENCE
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PRT;
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PROSITE: PSO(0260; GLUCAGON; 2.
PFAM; PF(0123; hormone2; 2.
HSSP; P01274; IGCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 DVSSYLQDQAAKDFVSWLKAG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14171 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.1%;
larity 38.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       24
49
80
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52
89 1
122 AA;
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SEQUENCE FROM N.A.
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P16455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Matches
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                                                                                                                                                   CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEOPTERYGII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00260; GLUCAGON; 2.
PFAM, PPOUL23; hormone2; 2.
GLUCAGON PAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

YUEN T.T.H., MOK P.Y., CHOW B.K.C.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.

-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOPHIIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE; 86286913.
NOE B.D., ANDREWS P.C.;
"Specific glucagon-related peptides isolated from anglerfish islets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LUND P.K., GOODMAN R.H., MONIMINY M.R., DEE P.C., HABENER J.F.;
"Anglerfish islet pre-proglucagon II. Nucleotide and corresponding amino acid sequence of the cDNA.";
J. BIOL. CHEM. 258:3280-3284(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRPP (GLICENTINE RELATED POLYPEPTIDE). GLUCAGON.
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15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
GLUCAGON II PRECURSOR.
LOPHIUS AMERICANUS (AMERICAN GOOSEFISH) (ANGLEREISH).
BUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; IELEOSTEI; EUTELEOSTEI; PARACANTHOPTERYGII; LOPHIIFORMES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are metabolic cleavage products of (pre)proglucagon-II.";
PEPTIDES 7:331-339(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 75; DB 1; Length 121,
Pred. No. 8.51e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLUCAGON-LIKE PEPTIDE DDB662CE CRC32;
                                                                        01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 AA.
                                      121 AA.
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                                      PRT;
                                                                                                                                                                                                             CYPRINIDAE; CYPRININAE; CARASSIUS
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13527 MW;
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39.1%;
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nes 9; Conservative
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                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AA;
                                                                                            01-NOV-1997 (REL. 3:
01-NOV-1997 (REL. 3:
GLUCAGON PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 83135785.
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                                  GLUC_CARAU
P79695;
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P04092;
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PEPTIDE
SEQUENCE
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Matches
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01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-UN-1994 (REL. 29, LAST ANNOTATION UPDATE)
METHYLATED-DNA --PROTEIN-CYSTEINE METHYLITRANSFERASE (EC 2.1.1.63) (6-0-METHYLGUANINE-DNA METHYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.
    AND RAISES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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"Isolation and structural characterization of a cDNA clone encoding
the human DNA repair protein for 06-alkylquanine.";
PROC. NATL. ACAD. SCI. U.S.A. 87:686-690(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRPP (GLICENTINE RELATED POLYPEPTIDE).
                                                                    -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KOIKE G., MAKI H., TAKEYA H., HAYAKAWA H., SEKIGUCHI M.; "Purification, structure, and biochemical properties of human O6-methylguanine-DNA methyltransferase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RYDBERG B., SPURR N., KARRAN P.;
"CDNA cloning and chromosomal assignment of the human of conethylguanine-DNA methyltransferase. CDNA expression in Escherichia coll and gene expression in human cells.";
J. BIOL. CHEM. 265:9563-9569(1990).
FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, THE BLOOD SUGAR LEVEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 75; DB 1; Length 122;
Pred. No. 8.51e-01;
'''..matches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLUCAĞON II.
GLUCAĞON-LIKE PEPTIDE II.
DFE63061 CRC32;
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[2]
SEQUENCE F
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      셤
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                                                                                                                           MEDLINE; 94261426.

LIEM L.-K., LIM A., LI B.F.L.;

Specificities of human, rat and E. coli 06-methylguanine-DNA methyltransferases towards the repair of 06-methyl and 06-ethylguanine in DNA.";

NUCLEIC ACIDS RES. 22:1613-1619-1994).

-!- FUNCTION: REPAIR 0F ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY TRANSFERRING THE ALKYL GROUP AI THE 0-6 POSITION TO A CYSTEINE RESIDUE IN THE BROXYME. THIS IS A SUICIDE REACTION: THE BROXYME IS
                                                                                                                                                                                                                                                                                                                                                                                              L-CYSTEINE.
SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLTRANSFERASE
HAYAKAWA H., KOIKE G., SEKIGUCHI M.; "Expression and cloning of complementary DNA for a human enzyme that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLIVES B., NEAU P., BAILLY P., HEDIGER M.A., ROUSSELET G., CARTRON J.-P., RIPOCHE P.; "Cloning and functional expression of a urea transporter from human
                                                                                                                                                                                                                                                                                                                            IRREVERSIBLY INACTIVATED.

CATALYTIC ACTIVITY: DNA (CONTAINING O6-METHYLGUANINE) + PROTEIN

L-CYSTEINE = DNA (WITHOUT O6-METHYLGUANINE) + PROTEIN S-METHYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALKYL GROUP ACCEPTOR (BY SIMILARITY).
A -> T (IN REF. 2).
397A1C19 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EJKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 75; DB 1; Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 8.51e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UT1_HUMAN STANDARD; PRT; 389 AA. Q13336, UV1_HUWAN STANDARD; PRT; 389 AA. Q1336, UNOV-1997 (REL. 35, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UKEA IKANSPORTER, ERYTHROCYTE.
SLC14A1 OR UT1 OR HUT11 OR UTE OR UK OR RACH1
HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA REPAIR; TRANSFERASE; METHYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. BIOL. CHEM. 269:31649-31652(1994)
                                             repairs O6-methylguanine in DNA.";
J. MOL. BIOL. 213:739-747(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A34889; XUHUMC.
MIM; 156569; -.
PROSITE: PSO0374; MGMT; 1.
PFRM; PF01035; Methyltrans; 1.
HSSP; P06134; 1SFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 145 P
127 127 P
207 AA; 21646 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.1%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X54228; G34559; -.
EMBL; M29971; G307199; -.
EMBL; M31767; G181616; -.
EMBL; M60761; G187579; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 WLKGAGATSGSPPAG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 wlknggpssgappps 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
MEDLINE; 95081111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone marrow cells.
                                                                                                              CHARACTERIZATION.
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä
                                                                                                                                                                                                             OLIVES B., MERRIMAN M., BAILLY P., BAIN S., BARNETT A., TODD T., CARTRON J.-P., MERRIMAN T.;

"The molecular basis of the Kidd blood group polymorphism and its lack of association with type I diabetes susceptibility.";

HUM. MOL. GENET. 6:1017-1020(1997).

-I- FUNCTION: SPECIALIZED LOW-AFFINITY UREA TRANSPORTER. MEDIATES UREA TRANSPORT IN ERTHROCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: ERYTHROCYTES.
-!- POLYMORPHISM: SLC14A1 IS RESPONSIBLE FOR THE KIDD BLOOD GROUP
--- SOLYMORPHISM: SLC14A1 IS RESPONSIBLE FOR THE KIDD BLOOD GROUP
--- SYSTEM. THE MOLECULAR BASIS OF THE JK(A)/JK(B) BLOOD GROUP
--- ANTIGENS IS A SINGLE VARIATION IN POSITION 280; ASP-280
CORRESPONDS TO JK(A) AND ASN-280 TO JK(B).
SEQUENCE FROM N.A.
MEDLINE; 96117053.
DAVER S., BERCH D.;
"RACH2, a novel human gene that complements a fission yeast cell
cycle checkpoint mutation.";
MOL. BIOL. CELL 6:1411-1421(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST ANDATICN UPDATE)
15-JUL-1998 (REL. 36, LAST ANDATION UPDATE)
HYPOTHETICAL 47.8 KD PROTEIN IN CSTA-DSBG INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 75; DB 1; Length 389;
Pred. No. 8.51e-01;
8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D -> N (IN JK(B)).
E -> K (IN REF. 1).
G -> GVG (IN REF. 1).
7; 17DC7F5A CRC32;
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                                                                                                                                                                   SEQUENCE FROM N.A., AND VARIANT JK(B) MEDLINE; 97358573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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EMBL; U35735; G1322222; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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78
1116
1143
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2243
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YBDN_ECOLI
P77216;
15-JUL-1998 (
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                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE E., ALLEN E., ARAUJO R., APARICIO A., DAVIS K., DUNCAN M.,
FEDERSPIEL N., HYMAN R., KALMAN S., KOMP C., KURDI O., LEW H., LIN D.,
NAMATH A., OEFNER P., ROBERTS D., SCHRAMM S., DAVIS R.W.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
SEQUENCE FROM N.A.

STRAIN-KIZ / MG1655,

MEDLINE; 97426617.

BLATTARR F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,

RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,

GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,

MAU B., SHAO Y.;

"The complete genome sequence of Escherichia coli K-12.";

SCIENCE 277:1453-1474(1997).
```

Score 75; DB 1; Length 406; Pred. No. 8.51e-01; 4; Mismatches 6; Indels 406 AA; 47826 MW; 1DC71FAD CRC32; EMBL; AE000165; G1786818; -. EMBL; U82598; G1778520; -. ECOGENE; EG13533; YBDN. HYPOTHETICAL PROTEIN. Query Match Ecst Local Similarity 41.2%; Matches 7; Conservative SEQUENCE SO KEN

49 ELARQMGKKICVLFIDW 65

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Gaps

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1 dlskgmeeeavrlfiew 17

Search completed: Mon Oct 4 15:26:59 1999 Job time: 8 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 6.16 Seconds 274.526 Million cell updates/sec Mon Oct 4 15:27:16 1999; Run on:

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>MOHAM-312-CLAIM84.PEP (1-31) from moham312177.pep 220 1 dlskqmeeeavrlfiewlknggpssgappps ritle: Description: Perfect Score: Sequence:

31

PAM 150 Gap 11 Scoring table:

179066 segs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

natabase:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 32.713; Variance 59.599; scale 0.549 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ssuit No. Sc	Score	Query					, CM
 H O W		Match	Length DB	DB	ID	Description	FIGU. INC.
C1 W	110	50.0	266	13	042143	PROGLUCAGON I.	7.43e-06
m	105	47.7	219	13	042144	PROGLUCAGON II.	5,34e-05
	95	43.2	2127	14	057294	L PROTEIN, RNA DEPENDE	2.47e-03
4	91	41.4	379	7	085863	HYPOTHETICAL 42.3 KD P	1.09e-02
5	98	39.1	552	6	038064	REPLICASE.	6.70e-02
9	11	35.0	99	13	091188	GLUCAGON (FRAGMENT).	1.53e+00
7	77	35.0	72	13	091409	PROGLUCAGON (FRAGMENT)	1.53e+00
œ	11	35.0	72	13	091408	PROGLUCAGON (FRAGMENT)	1.53e+00
σ	77	35.0	178	13	091189	•	1.53e+00
10	11	35.0	178	13	091971	GLUCAGON I.	1.53e+00
11	16	34.5	300	Н	059151	300AA LONG HYPOTHETICA	2.14e+00
12	26	34.5	333	?	048538	INTEGRASE/RECOMBINASE.	2.14e+00
13	97	34.5	2185	m	012721	ACETYL COA CARBOXYLASE	2.14e+00
14	75	34.1	664	7	059339	ADENYLYL - SULPHATE REDU	2.98e+00
15	75	34.1	999	11	088807	PEPTIDYLARGININE DEIMI	2.98e+00
16	75	34.1	999	11	035117	PEPTIDYLARGININE DEIMI	2.98e+00
17	74	33.6	502	'n	922770	T25B9.7 PROTEIN.	4.14e+00
18	73	33.2	337	S	061798	C33E10.8 PROTEIN.	5.74e+00
19	73	33.2	396	14	056869	PUTATIVE VIRAL TEGUMEN	5.74e+00
20	73	33.2	461	'n	001974	CODED FOR BY C. ELEGAN	5.74e+00

5.74e+00 5.74e+00 5.74e+00 7.74e+00 7.9
NEUROFASCIN PRECURSOR. 1952AA LONG HYPOTHETIC NEUROSASCIN PRECURSOR. F26C24.9 PROTEIN. VOLTAGE-GATED CALCIUM PROGLUCAGON. FROGLUCAGON. ESTERASE. HYPOTHETICAL PROTEIN. AMYR GENE. MYIN PROTEIN. AMYR GENE. NITHALTE REDUCTASE. WINTALTE REDUCTASE. NITHALTY TYROSINE PHOSP POLYPEPTIDE. PROGLUCAGON. SIMILARITY TO THIOREDO T23H. 2 PROTEIN. CARBOXYEPPTIDA. CARBOXYEPPTIDA. CARBOXYEPPTIDA. CARBOXYEPPTIDA. CARBOXYEPPTIDA. INJELOPE GLYCOPROTEIN PETITIOTIARGINE DEIMI POLYPROTEIN. 123H. 12, 1D, 2A, 2B, 2 SERINE ESTERASE. SERINE ESTERASE.
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ALIGNMENTS

o A	042143	PRELIMINARY;	PRT;	266 AA.	
	042143; 01-JAN-1998	(TREMBLREL. 05,	CREATED)		
	01-JAN-1998 01-NOV-1998	(TREMBLREL. 05, (TREMBLREL. 08,	LAST SEQUENCE LAST ANN	LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE)	
	PROGLUCAGON XENOPUS LAEV	PROGLUCAGON I. XENOPUS LAEVIS (AFRICAN CLAWED FROG).	PED FROG)		
	EUKARYOTA; M	ETAZOA; CHORDATA	A; VERTEB	ATA; AMPHIBIA; BATRACHIA;	ANURA;
8	MESOBATRACHI	A; PIPOIDEA; PIE	PIDAE; XE	MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.	
X X	SEOUTINCE FROM N.A.	M N.A.			
×	MEDLINE; 973	97368292.			
86	IRWIN D.M., S.	IRWIN D.M., SATKUNARAJAH M., WEN Y., BRUBAKER P.L.,	WEN Y.	BRUBAKER P.L., PEDERSON R.A.,	
5 5	"The Xenopus	, proglucadon der		encodes novel GLP-1-like peptides wi	with
RI	insulinotrop	insulinotropic properties.";		•	
Z.	PROC. NATL.	PROC. NATL. ACAD. SCI. U.S.A.		94:7915-7920(1997).	
ž 6	EMBL; AFOU44	EMBL; AFOU4432; GZ3USUIS; DBOSTTR: DSOO260: GIHCAGON:	ıń		
ăă	PEAM; PF0012	PFAM; PF00123; hormone2; 5.	,		
S	SEQUENCE 2	266 AA; 30951 MW;		E6139A25 CRC32;	
Ma Be	Query Match Best Local Simi Matches 13;	Similarity 54.2%; 13; Conservative	Score 11 Pred. No 6; Mis	<pre>Score 110; DB 13; Length 266; Pred. No. 7.43e-06; 6; Mismatches 5; Indels 0; Gat</pre>	Gaps C
Dp	105 DVTQQLD	FIDME	S 128		
δy	l:: :: 1 dlskame	: : :)S 24		
SU	RESULT 2				
£	042144	PRELIMINARY;	PRT;	219 AA.	
Z,	042144;				
T E	01-JAN-1998 01-JAN-1998	(TREMBLREL. 05, (TREMBLREL. 05.	CREATED)	ED) SECUENCE UPDATE)	
i E i	01-NOV-1998	EMBLREL.	LAST ANN	ANNOTATION UPDATE)	
8888	PROGLUCAGON XENOPUS LAEV EUKARYOTA; MESOBATRACHI	PROGLUCAKON II. XENODUS LAEVIS (AFRICAN CLAMED FROG). EUKARYOTA, METAZOA; CHORDATA; VERTEBR MESOBATRACHIA; PIPOIDEA; XEN	WED FROG) A; VERTEB PIDAE; XE	ATA; AMPHIBIA; BATRACHIA; OPODINAE; XENOPUS.	ANURA;
N C	[1]				
F.	SEQUENCE FRO	FROM N.A.			

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EMBL; AF079317; G3378295; -.
HYPOTHETICAL PROTEIN; PLASMID.
SEQUENCE 379 AA; 42269 MW; ED0127FC CRC32;
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| dlskgmeeeavrlfiewlkn 20
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01,
08,
                                                                                     Query Match
Best Local Similarity 37.9%;
Matches 11; Conservative
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EMBL; X80191; G517241; -.
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Conservative
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                                                                                                                                                                                                                                                                                                                                              (TREMBLREL.
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Matches 8; Conserv
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TISSUE-PANCREAS;
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SEQUENCE
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Q38064
Q38064;
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Q91188
Q91188;
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                                                        "The Xenopus proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties.";
PROC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997).
EMBL; AF004433; G2305018;
PROSITE; PROSITE; PROSICOS. GIUCAGON; 3.
PREAM: PFO0123; hormone2; 4 55271 MW; 45C42A88 CRC32;
                                                                                                                                                                                                                                                                             Gaps
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                 CHILL D.M., SAIKUNARAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A., WHEELER M.B.;
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BACTERIA, PROTEOBACTERIA, ALPHA SUBDIVISION, ZYMOMONAS GROUP,
SPHINGOMONAS.
                                                                                                                                                                                                                                Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2127;
                                                                                                                                                                                                                            Score 105; DB 13; Length 219
Pred. No. 5.34e-05;
8; Mismatches 5; Indels
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43.2%; Score 95; DB 14; Length 212
Best Local Similarity 47.6%; Pred. No. 2.47e-03;
Matches 10; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AB009663; D1024994; -.
EMBL; AB009601; D1024989; -.
SEQUENCE 2127 AA; 242427 MW; 847321FB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
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085863;
01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 42.3 KD PROTEIN.
SPHINGOMONAS AROMATICIVORANS.
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| dlskqmeeeavrlfiewlknggps 24
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                                                                                                                                                                                                                              Query Match 47.7%;
Best Local Similarity 45.8%;
Matches 11; Conservative
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97368292
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GLUCAGON (FRAGMENT).
0NCORNINCHUS WYKISS (FALNDOW TROUT) (SALMO GAIRDNER!).
EUKARYCHA; METAZOA; CHORDARA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIBORE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLSTHOORN R.C.L., GARDE G., DAYHUFF T., ATKINS J.F., VAN DUIN J.;
"Nuclectide sequence of a single-stranded RNA phage from Pseudomonas
aeruqinosa: kinship to coliphages and conservation of regulatory RNA
structures.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                         Gaps
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IRWIN D.M., WONG J.;

"Irout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";

MOL. ENDOCRINOL. 9:267-277(1995).

EMBL: 019913; G736361; -.

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Score 91, DB 2; Length 379; Pred. No. 1.09e-02; 9; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.1%; Score 86; DB 9; Length 552;
45.0%; Pred. No. 6.70e-02;
vative 9; Mismatches 0; Indels
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Pred. No. 1.53e+00;
8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                     LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                 9; Mismatches
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ONCORHYNCHUS MYKISS (RAINBOW TROUT) (SALMO GAIRDNERI).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELBOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                                                                                  EUGRRYOTR, METALOA; CHORDATA, VERTEBRATA, ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
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TISSUE.INEFERINE.
MEDILINE: 95295739.
IRWIN D.M., WONG J.;
"Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
MOL. ENDOCRINOL. 9:267-277(1995).
EMBL: 019917, 6736355.
EMBL: S78475; 6999385.
PROSITE; PEOUZEO; GLUCAGON; 3.
                                                                                                                                                                                                                                                                                                                                 CT 11
059151 PRELIMINARX; PRT; 300 AA.
059151; 01-AUG-1998 (TREMBLREL. 07, IAST SEQUENCE UPDATE)
01-AUG-1999 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
300AA LONG HYPOTHETICAL TRANSCRIPTION INITIATION FACTOR IIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 77; DB 13; Length 178;
Pred. No. 1.53e+00;
8; Mismatches 5; Indels
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                                                                                       GLUCAGON II.
ONCORHYNCHUS MYKISS (RAINBOW TROUT) (SALMO GAIRDNERI).
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LAST ANNOTATION UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
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Pred. No. 1.53e+00;
8; Mismatches 5;
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SEQUENCE 178 AA; 20034 MW; 2056F963 CRC32;
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Best Local Similarity 38.1%;
Matches 8; Conservative
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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Best Local Similarity
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                 SOUR RESERVENCE OCCUSE THE SOURCE OF THE SOU
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PROGLUCAGON (FRAGMENT).
ONCORHYNCHUS MYRISS (RAINBOW TROUT) (SALMO GAIRDNERI).
EUKARYOTA: METAZOA: CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI: EUTELEOSTEI: PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
ONCORHYNCHUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDAȚA; VERTEBRAȚA; AȚTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
ONCORHYNCHUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 95295739.
IRNIN D.M., WONG J.,
WOOD GOOD TO STAND TO STAND TO STAND THE SPLICE SPLIC
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MEDILINE; 92295739.
IRWIN D.M., WONG J.;
IRWIN D.M., WONG J.;
Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
MOL. ENDOCRINOL. 9:267-277 (1995).
EMBL: S78473; G999383; -
PERML: S78473; G999383; -
PERML: PF00123; hormone2; 2.
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                                                                                                                                                                                                                       Q91409; Q91232;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1998 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PROGIACAGON (FRAGMENT).
ONCORHYNCHUS TSCHAWYISCHA (CHINOOK SALMON) (KING SALMON).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 77; DB 13; Length 72;
Pred. No. 1.53e+00;
8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 77; DB 13; Length 72; Pred. No. 1.53e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
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                                                                                                                                                                                    72 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                    PRT;
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                 1 dlskqmeeeavrlfiewlkng 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 AA; 8293 MW;
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38.1%;
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l dlskqmeeeavrlfiewlkng
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                                                                                                                                                                                    PRELIMINARY;
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SEQUENCE
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Q91408
Q91408;
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Matches
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AC 09
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Best Local Similarity
Watches 7; Conserv
      MEDLINE; 96086936
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Best Local 9
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Q59339
Q59339;
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088807;
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                                                                               STRAIN-OT3;
MEDLINE; 98344137.
KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
YAWAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAWA A., NAGAI Y.,
YAWAMOTO S., SEKINE M., OGUKA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OGUKU Y.,
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                      ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; LACTOBACILLACEAE;
LACTOBACILLUS.
                                                                                                                                                                                                                                                        "Complete Sequence and Gene Organization of the Genome of a
Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3.";
MAR RES. 5:55-76(1998).
EMBL; AP000006; D1031532; -.
PROSITE; PS00782; TFIIB; 2.
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01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
ACETYL COA CARBOXYLASE (EC 6.4.1.2) (ACETYL-COA CARBOXXLASE).
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USTILAGINOMYCETIDAE; USTILAGINALES; USTILAGINACEAE; USTILAGO.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 34.5%; Score 76; DB 1; Length 300; Local Similarity 50.0%; Pred. No. 2.14e+00; es 10; Conservative 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 76; DB 2; Length 333;
Pred. No. 2.14e+00;
9; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-WS58;
KLEIN J.R., HENRICH B.;
KLEIN J.R., GUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Z50864; G971481; --
PRAM; PF00589; Phage_integrase; 1.
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                               300 AA; 34097 MW; 6E17BB64 CRC32;
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5 qmeeeavrlfiewlknggpssga 27
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01-NOV-1996 (TREMBLREL. 01, L
01-NOV-1998 (TREMBLREL. 08, L
INTEGRASE/RECOMBINASE.
LACTOBACILLUS DELBRUECKII.
PLASMID PWSS8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.5%;
Best Local Similarity 30.4%;
Matches 7; Conservative
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    PYROCOCCUS HORIKOSHII
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                                                               SEQUENCE FROM N.A.
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Q12721
Q12721;
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Q48538
Q48538;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPEICH N., DAHL C., HEISIG P., KLEIN A., LOTTSPEICH F., STETTER K.
BAILEY A.M., KEON J.P.R., OWEN J., HARGREAVES J.A.;
"The ACCI gene, encoding acetyl-CoA carboxylase, is essential for growth in Ustilago maydis.",
MOL. GEN. GENET. 249:191-201(1995).
-!- CATALYTIC ACTIVITY: ATP + ACETYL-COA + HCO(3)(-) = ADP +
PROPAPATH + MALONYL-COA.
-!- COFACTOR: BIOTIN.
EMBL, 246886; G600098; -.
PFRAM: PF00289; CFSase_L_chain; 1.
PFRAM: PF00289; Carboxyl_trans; 1.
LIGASE.
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BACTERIA; PROIEOBACIERIA; DELIA SUBDIVISION; DESULFOVIBRIO.
                                                                                                                                                                                                                                                                                                     Score 76; DB 3; Length 2185; Pred. No. 2.14e+00; 8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 75; DB 2; Length 664;
Pred. No. 2.98e+00;
8; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
ADBNILLYL-SULPHATE REDUCTARE ALFA-SUBUNIT (EC 1.8.99.2)
(ADBNILLYLSULFATE REDUCTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAN DEN BERG W., VAN DONGEN W., HAGEN W.;
SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                               2185 AA; 240029 MW; 84AA60F1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   664 AA; 74627 MW; ED9E9E3E CRC32;
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STRAIN-HILDENBOROUGH NCIMB 8303;
MEDLINE; 94362893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REDUCED ACCEPTOR.
-1- COFACTOR: FAD; IRON.
EMBL; Z69372; E221398; -.
EMBL; E0890; FAD_binding_2; 1.
OXIDOREDUCTASE.
SEQUENCE 664 AA; 74627 MW; EI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           988
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Local Similarity 34.5%;
nes 10; Conservative
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| dlskqmeeeavrlfiew 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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DE PEPTIDYLARGININE DEIMINASE TYPE IV (EC 3.5.3.15)

DE (PROTEIN-ARGININE DEIMINASE).

OS RATTUS NORVEGICUS (RAT).

OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA: RODENTIA;

CSCIURGONATHI; MURIDAE; MURINAE: RATTUS.

RN [1]

RN SEQUENCE FROM N.A.

RA ISHIGAMI A., KURAMOTO M., YAMADA M., WATANABE K., SENSHU T.;

RA ISHIGAMI A., KURAMOTO M., TAMADA M., WATANABE K., SENSHU T.;

RA ISHIGAMI A., KURAMOTO M., TAMADA M., WATANABE K., SENSHU T.;

RT "Molecular cloning of two novel types of peptidylarginine deiminase
RT "Molecular cloning of two novel types of peptidylarginine deiminase
RT REARLINGYTE CATIVITY: PROTEIN L-ARGININE + H(2)0 - PROTEIN

CC -: CATALYTIC ACTIVITY: PROTEIN L-ARGININE + H(2)0 - PROTEIN

CC -: CATALYTIC ACTIVITY: PROTEIN L-ARGININE + H(2)0 - PROTEIN

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CO -: CATALYTIC ACTIVITY: PROTEIN L-ARGININE + H(2)0 - PROTEIN

CO -: CATALYTIC ACTIVITY: PROTEIN L-A
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Search completed: Mon Oct 4 15:27:33 1999 Job time : 17 secs.

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protein - protein database search, using Smith-Waterman algorithm dd ಸಂಪ್ಷ್ಣ...

MasPar time 11.75 Seconds 56.092 Million cell updates/sec Mon Oct 4 15:26:14 1999; Run on:

not generated. -bular output claim 82 (1-31) from moham312177.pep 231 1 hgegtftsdlskqmeeeavrlfiewlknggy 31 >MOHAM-312-CLAIM82B.PEP pescription:
Perfect Score:
Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues

Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part39 31:part31 32:part37 38:part33 34:part35 36:part36 37:part37 38:part38

Mean 24.523; Variance 105.941; scale 0.231

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.93e-12	2.44e-11	2.44e-11	2.44e-11	2.44e-11	2.44e-11	2.44e-11	1.06e-10	1.06e-10	1.06e-10	1.06e-10	3.03e-10	4.60e-10	4.60e-10	4.60e-10	6.99e - 10
Description	Heloderma suspectum e	Exendin-4 $(1-30)$ for	Heloderma suspectum e	Heloderma suspectum e	Exendin-4, for use in	Gila monster exendin-	Heloderma suspectum p	H. horridum exendin-4	Exendin-3, for use in	Gila monster exendin-	Heloderma horridum ex	H. horridum exendin-4	Exendin-4 (1-28) amid	H. horridum exendin-3	H. horridum exendin-3	H. horridum exendin-4
Gi	R80544	W61771	R80543	R80546	W61770	W47609	W7028B	W39302	W61769	W47608	R80545	W39309	W61772	W39368	W39301	W39312
DB	14	39	14	14	39	30	35	29	39	30	14	29	39	29	29	29
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% Query Match	100.0	94.8	94.8	94.8	94.8	94.8	94.8	91.8	91.8	91.8	91.8	9.68	88.7	88.7	88.7	87.9
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dum exendin-4 dum exendin-7 dum exendin-7 dum exendin-7 dum exendin-1	TT DITOYS
H. horridum	
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2002 2002 2001 2001 2002 2003 2003 2003	7
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ALIGNMENTS

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WELLY 95-262627/34.

Stimulating/inhibiting insulin release with exendin polypeptide(s) - Stimulating/inhibiting insulin release with exendin polypeptide(s) - for treating diabetes mellitus and preventing hyperglycaemia.

Claim 2, columns 13-14, 17pp; English.

RR0544 is the Heloderma suspectum exendin 4 residues 1-31, where the native Pro31 has been replaced with a Tyr residue. It is an insulinotropic peptide, and can therefore be used in the treatment of diabetes mellitus (types I or II), and for the prevention of hyperglycaemia. It normalises hyperglycaemia through glucose-dependent and insulin-(in)dependent mechanisms.
R80544 standard; peptide; 31 AA.
R80544;
27-FEB-1996 (first entry)
Helodorma suspectum exendin-4 residues 1-31-Tyr31.
Exendin-4; residues 1-31; Y-31-Exendin-4(1-31); diabetes mellitus; hyperglycaemia; Tyr31; insulinotropic peptide.
                                                                                                                                                                                  24-MAY-1993; 066480.
24-MAY-1993; US-066480.
(ENGJ/) ENG J.
                                                                                                                          Heloderma suspectum.
US5424286-A.
                                                                                                                                                                 13-IUN-1995
                                                                                                                                                                                                                                             Eng J;
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; Score 231; DB 14; Length 31 Pred. No. 1.93e-12; 0; Mismatches 0; Indels 1 hgegtftsdlskqmeeeavrlfiewlknggy 31 Query Match
Best Local Similarity 100.0%;
Matches 31; Conservative

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Gaps

Length 31;

셤 ò RESULT 2
ID W61771; standard; peptide; 30 AA.
AC W61771;
DT 29-MAR-1999 (first entry)
DE Exendin-4 (1-30) for use in treating disorders related to food intake.

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WPI; 95-262627/34.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cating disorders and insulin resistance of the disperse.

cating disorders and insulin resistance claims 19, 26; page 11, 214pp; English.

The invention relates to an wethod for treating disorders that are alleviated by reducing food intake, in particular obesity, type II diabetes, eating disorders, insulin resistance syndrome, elevated plasma glucose levels, or the risk of cardiac disease. The method comprises administering an exendin or an exendin agonist. The treatment reduces appetite and lowers plasma lipid levels. It inhibits food consumption as effectively as amylin or cholecystokinin but has a much longer-lasting action (still effective after 6 hours in a mouse model). The present sequence is that of exendin-4 (1-30) or its amide which is one of the preferred compounds for use in the method.
Exendin; obesity; type II diabetes; eating disorders; cardiac disease; insulin resistance syndrome; elevated plasma glucose level; agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                         /note= "optionally the C-terminal is in amide form"
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Exendin-4; residues 1-31; Exendin-4(1-31); diabetes mellitus; hyperglycaenia; insulinotropic peptide.
Heloderma susparerum
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Pred. No. 2.44e-11;
...matches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reducing food intake by administering exendins or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 hgegtftsdlskqmeeeavrlfiewlkngg 30
                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         (AMYL-) AMYLIN PHARM INC.
Beeley NRA, Bhavsar S, Prickett KS;
WPI; 98-398796/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R80543 standard; peptide; 31 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R80543;
27-FEB-1996 (first entry)
Heloderma suspectum exendin-4
Exendin-4; residues 1-31; Exen
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Best Local Similarity 100.0%;
Matches 30; Conservative
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Best Local Similarity 100.0%;
Matches 30; Conservative
                                                                                                                                                                                                                     16-JUL-1998.

14-NOV-1997; US-066029.

07-JAN-1997; US-056029.

07-JAN-1997; US-034905.

08-AUG-1997; US-055404.

14-NOV-1997; US-055442.
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24-MAY-1993; 066480.
24-MAY-1993; US-066480.
                                                               Heloderma suspectum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heloderma suspectum.
USS424286-A.
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                                                                                                                           Modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Matches
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Deeley NRA, Bhavasa S, Prickett KS;

Beeley NRA, Bhavasa S, Prickett KS;

WPI; 98-398796/34.

Reducing food intake by administering exendins or their

Reducing food intealment of e.g. obesity, type II diabetes,

analogues - for treatment of e.g. obesity, type II diabetes,

cating disorders and insulin resistance

Claims 17, 25, Page 8; 214pp; English.

The invention relates to a new method for treating disorders that

The invention relates to a new method for treating disorders that

I diabetes, eating disorders, insulin resistance syndrome, elevated

II diabetes, and indiagonal and invention and exendin agonist. The treatment

reduces appetite and lowers plasma lipid levels. If inhibits fod

consumption as effectively as amylin or choleestokinin but has a much

longer-lasting action (still effective after 6 hours in a meuse model).

The present sequence is that of exendin-4 which is one of the preferred

compounds for use in the method.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Columns 13-14; 17pp; English.
R80546 is Heloderma suspectum exendin-4. It is an distull notropic peptide, and can therefore be used in the treatment of diabetes mellitus (types I or II), and for the prevention of hyperglycaemia. It normalises hyperglycaemia through glucose-dependent sed insulin-(in)dependent mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-1999 (first entry)
Exendin-4, for use in treating disorders related to food intake.
Exendin; obesity; type II diabetes; eating disorders; cardiac disease; insulin resistance syndrome; elevated plasma glucose level; agonist.
                                                                                       27-FEB-1996 (first entry)
Heloderma suspectum exendin-4.
Exendin-4; diabetes mellitus; hyperglycaemia; insulinotropic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stimulating/Inhibiting insulin release with exendin polypeptide(s) for treating diabetes mellitus and preventing hyperglycaemia. Claim 6; Columns 13-14; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Pred. No. 2.44e-11;
0; Mismatches 0; Indels
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Pred. No. 2.44e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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W61770 standard; peptide; 39 AA.
                                  Ā
T
R80546 standard; peptide; 39
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Best Local Similarity 100.0%;
Matches 30; Conservative
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Best Local Similarity 100.0%;
Matches 30; Conservative
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07-JAN-1997; US-034905.
08-AUG-1997; US-055404.
14-NOV-1997; US-065442.
(AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                              24-MAY-1993; 066480.
24-MAY-1993; US-066480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heloderma suspectum.
WO9830231-A1.
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14-NOV-1997; US-066(
                                                                                                                                                                                               Heloderma suspectum
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 95-262627/34
                                                                                                                                                                                                                                                                                                                                                                (ENGJ/) ENG J.
                                                                                                                                                                                                                                  US5424286-A.
                                                                                                                                                                                                                                                                  13-JUN-1995.
                                                                  R80546;
                                                                                                                                                                                                                                                                                                                                                                                                      Eng J
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                               HD DAY ON MAC ON THE STATE OF T
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Gaps

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NPT: 98-447230/38.

N-PSDB; v33163.

The modorine tumours, also to treat poisoning by reptile venom claim 3; Fig 2; 26pp; English.

The meloderma suspectum prockendin peptide is encoded by its cDNA which was isolated from a H. suspectum salivary gland cDNA library. The proexendin protein comprises of a novel exendin A peptide ENTY.

The proexendin protein comprises of a novel exendin N-terminal consensus dipeptidyl peptidase cleavage site. The proexendin conn. identify related sequences (e.g. the care of Heloderma horridum, mutant alleles and proexendin connected with metabolic disease) and species homologues (e.g. for developing animal models for drug screening). The proexendin peptide can be used to raise antibodies. Anti-proexendin can be used to raise antibodies. Anti-proexendin with altered levels of proexendin (e.g. endocrine tumours and organ failure), for identifying other regulators of cell metabolism, in drug screens and for treating metabolic diseases (e.g. diabetes) and for neutralising, or detecting, reptilian venom peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Truncated versions of exendin peptide(s) for treating diabetes -
increase secretion and biosynthesis of insulin, but reduce those of
juccagon, and do not induce hypoglycaemia
glucagon, and do not induce hypoglycaemia
This peptide is a fragment of exendin-4 isolated from Heloderma
This peptide and its salts, esters and derivatives can be
used to treat diabetes mellitus. They stimulate biosynthesis and
secretion of insulin, but have the opposite effect on glucagon, and
independent of this activity can increase peripheral glucose utilisation.
Exendin-3 and exendin-4 are only active when blood sugar levels are
high, so they will not induce hypoglycaemia. Compared with glucagon-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "This residue can be any amino acid except Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. horridum exendin-4 peptide.
Exendin-3; exendin 4; diabetes; insulin; secretion; biosynthesis;
glucagon reduction; hypoglycaemia; glucose; treatment.
                                           46..47
/note= "Dipeptidyl peptidase cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 219; DB 35; Length 87
Pred. No. 2.44e-11;
0; Mismatches 0; Indels
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                     "Exendin 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BOEF ) BOEHRINGER MANNHEIM GMBH. Goeke B, Goeke R, Hoffmann E; WPI; 98-042119/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .r 8
W39302 standard; peptide; 30 AA.
W39302;
05-JUN-1998 (first entry)
                                                                                                                                                           OD-FEB-1997; US-037412.
(ONEO-) 1149336 ONTARIO INC.
Drucker DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 94.8%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30; Conservative
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13-SEP-1996; DE-037230.
05-JUN-1996; DE-022502.
48..87
/note-
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                                                                                                                                     04-FEB-1998; CA0071
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                                              Cleavage_site
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  Peptide
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0
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WPI: 98-145351/13.
Regulating gastrointestinal motility using exendins or their
agonists - for treating spasm, diabetic postprandial hyperglycaemia,
impaired glucose tolerance etc., also in diagnostic investigations
Claims 20 and 21; Fig 1; 70pp; English.
WA7749 describes a generic exendin agonist, provided that it does
have the formula of either exendin-3 (W47608) or exendin-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exendin agonists, which reduce gastric motility and delay gastric emptying, can be used to treat spasm (where associated with acute diverticulitis or disorders of the biliary tract or sphincer of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type I diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic resonance
                                                                                                                                                                                                                                 Exendin agonist; gastric motility; gastric emptying; treatment; spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity; Gila monster venom; exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US3424286) for treatment of diabetes and prevention of hyperglycaemia.
Sequence 39 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exendins, components of Gila monster venom, have some sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
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1..47
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Heloderma suspectum proexendin peptide.
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  30
                        Location/Qualiflers
  1 hgegtftsdlskgmeeeavrlfiewlkngg
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                                                                                                   JT 6
W47609 standard; peptide; 39
W47609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 30; Conservative
                                                                                                                                                                                        03-JUL-1998 (first entry) Gila monster exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-AUG-1996; US-694954.
(AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                              Heloderma suspectum
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Gaps

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Length 87;

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WPI; 98-386796/34.

**Reducing food intake by administering exendins or their analogues - for treatment of e.g. Obesity, type II diabetes, and losulin resistance and insulin resistance.

PT claims 16, 24; Page 8; 214pp; English.

The invention relates to a new method for treating disorders that a livention relates to a new method for treating disorders, type of a lleviated by reducing food intake, in particular obesity, type of li diabetes, eating disorders, insulin resistance syndrome, elevated plasma glucoses levels, or the risk of cardiac disease. The method comprises administering an exendin or an exendin agonist. The treatment consumption as effectively as amylin or cholecystokinin but has a much longer-lasting action (still effective after 6 hours in a mouse model).

The present sequence is that of exendin-3 which is one of the preferred
peptide 1 (GLP1) and the known exendins, they are more active (effective at lower doses), more stable to degradation and metabolism and have a longer lasting effect. Truncated forms of this peptide can be made more economically than full length versions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-1999 (first entry)
Exendin-3, for use in treating disorders related to food intake.
Exendin, obesity; type II diabetes; eating disorders; cardiac disease; insulin resistance syndrome; elevated plasma glucose level; agonist.
                                                                                                                                                                                                                                                                              0; Gaps
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Pred. No. 1.06e-10;
2; Mismatches 0; Indels
                                                                                                                                                                                               Query Match 91.8%; Score 212; DB 29; Length 30; Best Local Similarity 100.0%; Pred. No. 1.06e-10; Matches 29; Conservative 0; Mismatches 0; Indels
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W61769 standard; peptide; 39
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Best Local Similarity 93.3%;
Matches 28; Conservative
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US-034905.
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                                                                                  economically than
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12-FEB-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for treating diabetes mellitus and preventing hyperglycaemia.
Claim 5; Columns 13-14; 17pp; English.
R80545 is Heloderma horridum exendin-3. It is an
insulinotropic peptide, and can therefore be used in the treatment of
diabetes mellitus (types I or II), and for the prevention of
hyperglycaemia. It normalises hyperglycaemia through glucose-dependent
and insulin-(in)dependent mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heloderma horridum exendin-3.
Exendin-3; diabetes mellitus; hyperglycaemia; insulinotropic peptide.
Heloderma horridum.
                                               Beeley NRA, Gedulin B, Prickett KS, Young AA;
WPI; 98-14535/13.
Regulating gastrointestinal motility using exendins or their
Regulating gastrointestinal motility using exendins or their
agonists - for treating spasm, diabetic postprandial hyperglycaemia,
impalred glucose tolerance etc., also in diagnostic investigations
Claims 20 and 21; Fig 1; 70pp; English.
W47549 describes a generic exendin agonist, provided that it does
W47609).
W47609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                      Exendin agonists, which reduce gastric motility and delay gastric emptying, can be used to treat spasm (where associated with acute diverticulities or disorders of the bilary tract or sphincter of oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is intestines, then the stomach pumped) and obesity. They can also be administered to subjects undergoing gastrointestinal diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 95-262627/34.
Stimulating/inhibiting insulin release with exendin polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                        investigation, particularly radiological or by magnetic resonance
                                                                                                                                                                                                                                                                                                                                                                                                                      similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.
                                                                                                                                                                                                                                                                                                                                                                                                           have some sequence
They are GLP agonia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 212; DB 30; Length 39;
Pred. No. 1.06e-10;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 212; DB 14;
Pred. No. 1.06e-10;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                    components of Gila monster venom, v to qlucaqon-like peptides (GLP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 hsdgtftsdlskqmeeeavrlfiewlkngg 30
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ID W39309 standard; peptide; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R80545 standard; peptide; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.8%;
ilarity 93.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 91.8%;
Similarity 93.3%;
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-FEB-1996 (first entry)
08-AUG-1997; U14199.
08-AUG-1996; US-694954.
(AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-UUN-1933.
24-MAY-1993; 066480.
24-MAY-1993; US-066480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ENGJ/) ENG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5424286-A.
                                                                                                                                                                                                                                                                                                                                                                                                           Exendins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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11-DEC-1997.
05-JUN-1997; E02930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heloderma horridum.
                                                                                                                             28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified_site
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                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W39368;
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                                                                                                                                                                                                                                                       DITECTION.

11-DEC-1997; E02930.

PRE 05-JUN-1997; E02502.

PR 13-SEP-1996; DE-0372502.

PA (BOEF ) BOEHRINGER MANNHEIM GMBH.

GOKEE B, Gocke R, Hoffmann E;

MPI: 98-042119/04.

PI TRUNCATE OF VERSIONS of exendin peptide(s) for treating diabetes -

increase secretion and biosynthesis of insulin, but reduce those of

Truncated versions of exendin peptide(s) for treating diabetes -

Slucagon, and do not induce hypoglycaemia

Peptides w39303-w39420 are fragments of exendin-3 and exendin-4

isolated from Heloderma horridum which are used in a novel method

for the treatment of diabetes mellitus. These peptides can stimulate

CC qlucagon, and independent of this activity can increase peripheral

CG glucagon, and independent of this activity can increase peripheral

CG glucagon, ind independent of this activity can increase peripheral

CG glucagon, ind independent of this activity can increase peripheral

CG glucagon, ind independent of this activity can increase peripheral

CG glucagon, ind independent of this activity can increase peripheral

CG glucagon, ind independent of this activity can increase peripheral

CG glucagon, and independent of this activity can increase peripheral

CG glucagon, and independent of this activity can increase peripheral

CG glucagon, and independent of this activity can increase peripheral

CG glucagon, and independent of peripheral

CG sugar levels are high, so they will not induce hypoglycaemia. Compared

CC metabolism and have a longer lasting effect. Truncated forms of this

CG peptide can be made more economically than full length versions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Claims 18, 26; Page 12; 214pp; English.

The invention relates to a new method for treating disorders that are alleviated by reducing food intake, in particular obesity, type II diabetes, eating disorders, insulin resistance syndrome, elevated plasma glucose levels, or the risk of cardiac disease. The method comprises administering an exendin or an exendin agonist. The treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-WAR-1999 (first entry)
Exendin-4 (1-28) amide for use in treating disorders related to food.
Exendin; obesity, type II diabetes; eating disorders; cardiac disease;
insulin resistance syndrome; elevated plasma glucose level; agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                  H. horridum exendin-4 peptide derivative #6.
Exendin-3; exendin 4; diabetes; insulin; secretion; biosynthesis;
glucagon reduction; hypoglycaemia; glucose; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                           /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-NOV-1997; US-066029.
07-JAN-1997; US-056029.
08-AUG-1997; US-055404.
14-NOV-1997; US-055404.
(AMYL-) AMYLIN PHARM INC.
Beeley NRA, Bhavar S, Prickett KS; WPI; 98-398796/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .T 13
861772 standard; peptide; 28 AA.
W61772:
29-WAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 96.6%;
Matches 28; Conservative
                      05-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUL-1998,
07-JAN-1998; U00449.
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                                                                                                                                     Heloderma horridum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 AA;
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Modified_site
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ID W6
AC W6
DT 29
DT 29
KW EX
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plucagon, and do not induce hypoglycaemia claim 2; Page 27; 150pp; English.

Claim 2; Page 27: 150pp; English.

Peptides wy3303 wy3420 are fragments of exendin-3 and exendin-4 isolated from Heloderma horridum which are used in a novel method for the treatment of diabetes mellitus. These peptides can stimulate biosynthesis and secretion of insulin, but have the opposite effect on glucagon, and independent of this activity can increase peripheral glucose utilisation. Exendin-3 and exendin-4 are only active when blood sugar levels are high, so they will not induce hypoglycaemia. Compared active (effective at lower doses), more stable to degradation and metabolism and have a longer lasting effect. Truncated forms of this peptide can be made more economically than full length versions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
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                   consumption as effectively as amylin or cholecystokinin but has a much longer-lasting action (still effective after 6 hours in a mouse model). The present sequence is that of exendin-4 (1-28) amide which is one of the preferred compounds for use in the method.
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Truncated versions of exendin peptide(s) for treating diabetes -
increase secretion and biosynthesis of insulin, but reduce those of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-1998 (first entry)
H. horridum exendin-3 peptide derivative #11.
Exendin-3; exendin 4; diabetes; insulin; secretion; biosynthesis; glucagon reduction; hypoglycaemia; glucose; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W39301;
05-JUN-1998 (first entry)
Exendin-3 peptide.
Exendin-3; exendin 4; diabetes; insulin; secretion; biosynthesis; glucagon reduction; hypoglycaemia; glucose; treatment.
Heloderma horridum.
reduces appetite and lowers plasma lipid levels. It inhibits food
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                                                                                                                                                                                                                 Length 28;
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Pred. No. 4.60e-10;
2; Mismatches 0;
                                                                                                                                                                                                                 Score 205; DB 39;
Pred. No. 4.60e-10;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                              | hgegtftsdlskgmeeeavrlfiewlkn 28
                                                                                                                                                                                                                                                                                                                                              1 hgegtftsdlskgmeeeavrlfiewlkn 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-1996; DE-037230.
05-JUN-1996; DE-022502.
GOEK B. GOEKE MANNHEIM GMBH.
GOEKE B. GOEKE R. HOffmann E;
WPI; 98-042119/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 14
W39368 standard; peptide; 30 AA.
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Best Local Similarity 93.1%;
Matches 27; Conservative
                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 28; Conservative
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WO9746584-Al

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PF 11-DEC-1997; E02930.

PR 13-SEP-1996; DE-037230.

PR 13-SEP-1996; DE-037230.

PR 05-JUN-1997; E02930.

PR 05-JUN-1996; DE-022562.

PR 05-JUN-1996; DE-022562.

PR 05-JUN-1996; DE-022562.

PR (BOEF ) BOEHRINGER MANNHEIM GMBH.

PI GOOKE B, Gooke R, Hoffmann E;

PR 11-DEC-1996; DE-022562.

PR 05-JUN-1996; DE-022562.

PR (BOEF ) BOEHRINGER MANNHEIM GMBH.

PI GOOKE B, Gooke R, Hoffmann E;

PR (BOEF ) BOEHRINGER MANNHEIM GMBH.

PR 10-Cadon, and do not induce hypoglycaemia

Claim 1; Page 3; 150pp; English.

Claim 1; Page 3; 150pp; English.

Claim 1; Page 3; 150pp; English.

Contridum. This peptide and its salts, esters and derivatives can be care to treat diabetes mellitus. They stimulate biosynthesis and independent of this activity an increase peripheral glucose utilisation.

Exendin-3 and exendin-4 are only active when blood sugar levels are compared with glucagon-like Exendin-3 and exendin-4 he known exendins, they are more active (effective at lower doses), more stable to degradation and metabolism and have a connence at lower doses), more stable to degradation and metabolism and have a connence at lower doses), more stable forms of this peptide can be made more connence at lower doses.

PR (BOEF ) and this known exendins of this peptide can be made more connence at lower doses).

PR (BOEF ) and this length versions.
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; 0 Score 205; DB 29; Length 30; Pred. No. 4.60e-10; 2; Mismatches 0; Indels Query Match
Best Local Similarity 93.1%;
Matches 27; Conservative economically than sequence 30 AA;

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Gaps

1 hsdgtftsdlskqmeeeavrlfiewlkng 29

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Search completed: Mon Oct 4 15:26:33 1999
Job time : 19 secs.

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Release 3.1A John F. Collins, Blocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Oct 4 15:25:48 1999; MasPar time 6.68 Seconds 185.964 Million cell updates/sec Run on:

bular output not generated.

>MOHAM-312-CLAIM82B.PEP (1-31) from moham312177.pep 231 1 hgegtftsdlskqmeeeavrlfiewlknggy 31 rtle: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

122810 seqs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pirl 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 34.253; Variance 64.514; scale 0.531 Statistics:

		ď			SUMMARIES		
Result		Query					
No.	Score	Match	Length DB	BB	ID	Description	Pred. No.
((219	94.8	98	Н	HWGH4G	exendin-4 - Gila mons	2.37e-25
. 5	212	91.8	39	-1	HWGH3Z	١	5.61e-24
m	127	55.0	31	~	S44472	G2 - North	3.78e-08
4	124	53.7	101	Н	GCFGB	qlucadon precursor -	1.24e-07
5	122	52.8	30	~	S44473	qlucadon-like peptide	2.73e-07
9	122	52.8	31	~	S44471		2.73e-07
7	121	52.4	30	~	C61125	ike	4.05e-07
8 0	121	52.4	30	7	B61125	glucagon-like peptide	4.05e-07
m	120	51.9	63	Н	GCIDC		5.99e-07
10	120	51.9	99	N	151093	glucagon - chinook sa	5.99e-07
11	120	ä	178	~	I51058	glucagon I precursor	5.99e-07
12	120	4	178	7	151057	Н	5.99e-07
£.	119	51.5	72	~	GCGXA	Ω	8.84e-07
14	118		122	Н	GCAF2	glucagon 2 precursor	1.30e-06
15	117	50.6	0.9	Н	GCONC	glucagon precursor -	1.92e-06
16	115	49.8	29	Н	GCDF	glucagon - smaller sp	4.16e-06
17	115		158	Н	GCPG	precursor	4.16e-06
18	115	49.8	180	~	A57294	glucagon precursor -	4.16e-06
19	115	49.8	180	Н	GCHY	glucagon precursor -	4.16e-06
ر. د.	115	•	180	~1	GCRIDU	glucagon precursor -	4.16e-06
21	115		180	Н	GCBO	glucagon precursor -	4.16e-06
22	115	49.8	180	Н	GCGP	glucagon precursor -	4.16e-06
23	115	49.8	180	Н	GCHU	glucagon precursor -	4.16e-06

glucagon precursor - 4.16e-06 glucagon precursor - 6.11e-06 glucagon - chicken 6.11e-06 glucagon - Chinchilla 2.80e-05 glucagon - marbled el 5.96e-05 glucagon - marbled el 5.96e-05 glucagon - bigeye tun 2.64e-04 glucagon precursor - 2.64e-04 glucagon precursor - 2.64e-04 glucagon - rabbit (te 1.15e-03 glucagon - common squ 1.15e-03 glucagon - bowfin 1.65e-03 glucagon - elephantfi 1.65e-03 glucagon - elephantfi 1.65e-03 glucagon - turkey (te 4.84e-03 glucagon - turkey (te 6.91e-03 glucagon - slider tur 6.91e-03 glucagon - duck	SEN	lete ter a suspectum #common_name Gila monster _revision 31-Mar-1993 #text_change	A.; Singh, L.; Singh, G.; Raufman, J.P. 267:7402-7405 erization of exendin-4, an exendin-3 derma suspectum venom. Further evidence ptor on dispersed acini from guinea pig	amylase secretion by pancreatic acinar	<pre>duplication; venom idated carboxyl end (Ser) #</pre>	r-Weight 4188 #checksum 95/0 :219; DB 1; Length 39; No. 2.37e-25; Mismatches 0; Indels 0; Gaps 0;	63 30 - 930	ete aded lizard horridum *common_name Mexican beaded revision 31-Mar-1993 *text_change ; Kleinman, W.A.; Singh, L.; Raufman,
GCCH GCCH GCCH GCCB GCCB GCCB AGIL135 GCFIS A91741 A91742 A91742 A91740 GCCBN GCCBN GCCBN GCCBN GCCBN GCCBN GCCBN GCCBN GCCBN GCCBN GCCCCBN GCCCBN GCCCCBN GCCCBN GCCCBN GCCCCBN GCCCCBN GCCCBN GCCCCBN GCCCBN GCCCBN GCCCBN GCCCC	ALIGNMENT	compl monst derma	n, W.A 1992) aracte Helod recep	8391 abel ENG stimulate	ago en te	scula Score Pred. 0;	HGEGTFTSDLSKQMEEBAVRLFIEWLKNG 	compl can be oderma uence_
HHAHHAHAHAAAHAHAH			Kleinma Chem. (and ch te, from	1218 #1a	rbo red rim	.08; 108; 1ve	WRLF vrlf	*type - Mexi. ame Hell 93 *seq 1997
011011 011011 011011 011011 011011 011011		GB4G #t endin-4 - G ormal_name -Mar-1993 #		ancreas. MUID:92218391 486 e protein 1-39 ##label does not stim	# × × × × × × × × × × × × × × × × × × ×		SKOMEEEAVR skqmeeeavr	32 31n-3 nal_n 2ard ar-19 -Nov- 74 J.;
844008000WWWWWWAAAA		HWGH4G exendin- #formal_ 31-Mar-]	A4248 A4248 Eng, J. Bit Isola	42 42 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	s. #sup amid	#lengt larity Conse	SDLS	HWGH3Z exendin #formal 11zar 21-Mar 21-No A23674 A23674 EDG, J.
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40000000000000004444444444000000000000		RESULT ENTRY TITLE ORGANISM	ACCESSIONS REFERENCE #authors #journal #title	#Cross - #access	CLASSIFICAT KEYWORDS FEATURE 39	SUMMAKY Query Ma Best Loc Matches	oy Oy	RESULT 2 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors

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Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.
Biochem. J. (1994) 300:339-345
Characterization of insulins and proglucagon-derived peptides
from a phylogenetically ancient fish, the paddlefish
(Polyodon spathula).
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glucagon-like peptide - North American paddlefish (Polyodon
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#label GL1\
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#label GL2
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                               the of
                         #title Isolation of peptide hormones from the pancreas of t
bullfrog (Rana catesbelana). Amino acid sequences
pancreatic polypeptide, oxyntomodulin, and two
glucagon-like peptides.
#cross-references MUID:88257102
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ن
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18-Sep-1997 #sequence_revision 18-Sep-1997
20-Mar-1998
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Pred. No. 1.24e-07;
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Pred. No. 2.73e-07;
7; Mismatches 6;
           J. Biol. Chem. (1988) 263:9746-9751
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duplication; hormone; pancreas
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##residues 37-68 ##label POL
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|hgegtftsdlskqmeeeavrlfiewlkng
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##residues 1-30 ##label NGU
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Best Local Similarity 51.7%;
Matches 15; Conservative
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Best Local Similarity 55.2%;
Matches 16; Conservative
                                                                                                                                ##molecule_type protein
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                                                                                 ##molecule_type protein
##residues 1-39 ##label ENG
##residues 1-39 ##label ENG
##residues 1-39 ##label ENG

NT Exendins are venom components that are thought to bind to receptor for vasoactive intestinal peptide and/or secretin on pancreatic actinar cells and to activate adenylate cyclase, resulting in secretion of amylase.

IFICATION #superfamily glucagon amidated carboxyl end; duplication; secretagogue; venom
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glucagon G2 - North American paddlefish (Polyodon spathula)
#formal_name Polyodon spathula
12-Mar-1997 #sequence_revision 12-Dec-1997 #text_change
S44472
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Pollock, H.G.; Hamilton, J.W.; Rouse, J.B.; Ebner, K.E.;
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#formal_name Rana catesbeiana #common_name bullfrog
31-Mar-1993 *sequence_revision 31-Mar-1993 *text_change
                                                                                                                                                                                                                                                             #modified_site amidated carboxyl end (Ser) #status
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Characterization of insulins and proglucagon-derived pefrom a phylogenetically ancient fish, the paddlefish (Polyodon spathula).
experimental #length 39 #molecular-weight 4204 #checksum 9591
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#length 31 #molecular-weight 3682 #checksum 7826
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Pred. No. 5.61e-24;
2; Mismatches 0; Indels
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glucagon precursor - bullfrog (fragments)
oxyntomodulin
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                                                                                                                                                                                                                                                                                                                                   91.8%;
ilarity 93.3%;
Conservative
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Best Local Similarity 55.2%;
Matches 16; Conservative
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##residues 1-31 ##]
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28; Conser
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KEYWORDS
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GCIDC
#type fragments
glucagon precursor - channel catfish (fragments)
#formal_name clalurus punctatus #common_name channel catfish
31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
20-Mar-1998
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Mol. Endocrinol. (1995) 9:267-277
Trout and chicken proglucagon: alternative splicing generates
#cross-references MUD:91340068
#accession B61125
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#product glucagon-like peptide 1 #status experimental
#label GL1
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#label GLP\
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predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andrews, P.C.; Ronner, P. J. Balol. Chem. (1985) 260:3910-3914 Isolation and structures of glucagon and glucagon-like peptide from catfish pancreas.
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                                                                                                                                                                                                                                                                                                 Query Match 52.4%; Score 121; DB 2; I
Best Local Similarity 48.3%; Pred. No. 4.05e-07;
Matches 14; Conservative 9; Mismatches 6;
                                                                                                                                *superfamily glucagon amidated carboxyl end; duplication
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                                                                                          ##molecule_type protein
##residues 1-30 ##label CON
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#accession A05166
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Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.
Biochem. J. (1994) 300:339-345
Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish
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#label GLP\
#modified_site amidated carboxyl end (Arg) #status
experimental
#length 30 #molecular-weight 3376 #checksum 6092
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#formal_name Anguilla rostrata #common_name American eel
10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C61125 *type complete
glucagon-like peptide - European eel
fformal.name Anguilla anguilla *common_name European eel
10.Mar-1994 *sequence_revision 10-Mar-1994 *text_change
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FICATION #superfamily glucagon
DS carbohydrate metabolism; duplication; hormone; pancreas
       18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change
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#length 31 #molecular-weight 3751 #checksum 7808
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Conlon, J.M.; Andrews, P.C.; Thim, L.; Moon, T.W.
Gen. Comp. Endocrinol. (1991) 82:23-32
                                                                                                                                                                                                                                                                                                                                                 Score 122; DB 2; Length 31;
Pred. No. 2.73e-07;
6; Mismatches 7; Indels
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amidated carboxyl end; duplication
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                                                                                                                                                   (Polyodon spathula).
S44471
                                                                                                                                                                                     ##molecule_type protein
##residues 1-31 ##label NGU
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Post Local Similarity 55.2%;
Watches 16; Conservative
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Best Local Similarity 44.8%;
Matches 13; Conservative
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#title Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2. #across-references MUID:95295739 #acrossion IS1058
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##nolecule_type iRNA
##residues 1-178 ##label IRW
##cross-references EMBL:U19917; NID:q736364; PID:q736365; GB:S78475;
##cross-references EMBL:U1999384; PID:q999385
                                                                                                                                                                                                                                                                                                                                                              151058 *type complete
glucagon I precursor - rainbow trout
#formal_name Oncorhynchus mykiss #common_name rainbow ti
13.5ep-1996 *sequence_revision 13-Sep-1996 *text_change
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mRNA transcripts encoding glucagon-like peptide 2. #cross-references MUID:95295739 #accession I51093
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duplication
#length 178 #molecular-weight 20034 #checksum
                                  ##status preliminary; translated from GB/EMBL/DDBJ ##molecule_type mRNA ##residues 1-66 ##label IRW ##cross-references EMBL:U19920; NID:9736366; PID:9736367 CLASSIFICATION #superfamily glucator
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A55895
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Pred. No. 5.99e-07;
11; Mismatches 5; Indels
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##residues /M',114-144 ##label IR4
##cross-references_EMBL:019919; NID:9736374; PID:9736377
                                                                                                                #superfamily glucagon
duplication
#length 66 #checksum 1440
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Best Local Similarity 44.8%;
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#authors Irwin, D.M.; Wong, J. #50urnal Mol. Endocrinol. (1995) 9:267-277
#title Trout and chicken proglucagon: alternative splicing generates mana transcripts encoding glucagon-like peptice 2. #across-references MulD:95295739
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glucagon; glucagon-36 (oxyntomodulin); glucagon-like peptide
151057 #type complete
glucagon II precursor - rainbow trout
#formal_name Oncorhynchus myxiss #common_name rainbow trout
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
21-Nov-1997
151039; 151039; 151038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Soldsay Farence, W.E.; Ebner, K.E.; Hamilton, J.W.; Rouse, J.B.; Lance, V.; Rawitch, A.B. Rouse, J.B.; Lance, V.; Rawitch, A.B. Gen. Comp. Endocrinol. (1988) 69:133-140 Isolation of alligator gar (Lepisosteus spatula) glucagon, oxyntomodulin, and glucagon-like peptide: amino acid sequences of oxyntomodulin and glucagon-like peptide. #accession S06339
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31.Mar-1993 #sequence_revision 31.Mar-1993 #text_change
20-Mar-1999
S06339; S06871
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carbohydrate metabolism; duplication; hormone; pancreas
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##cross-references EMBL:U19916; NID:9736369; PID:9736372
cession 151038
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##cross-references EMBL:U19915; NID:g736368; PID:g736371
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Pred. No. 5.99e-07;
11; Mismatches 5; Indels
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FEATURE
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#authors Plisetskaya, E.; Pollock, H.G.; Rouse, J.B.; Hamilton, J.W.;
Kimmel, J.R.; Gorbman, A.
#journal Regul. Pept. (1986)
#title Isolation and structure of coho salmon (oncorhynchus kisutch)
glucagon and glucagon-like peptide.
#cross-references MUID:86234328
#accession JP0103
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#product glucagon #status predicted #label GCN\,
#product glucagon-like peptide 1 #status predicted
#label Gl.
#label Gl.
#label Gl.
#label Gl.
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*product glucagon-like peptide 1 *status predicted
*label GL1
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##cross-references GB:J00933; NID:g213352; PID:g213353
FPICATION #superfamily glucagon
US carbohydrate metabolism; duplication; hormone; pancreas
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glucagon; glucagon-like peptide 1
#formal.name Oncorhynchus Kisutch #common_name coho saln
30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                        GCAF2 #type complete
glucagon 2 precursor - American goosefish
glucagon; glucagon-like peptide 1
#formal_name Lophius americanus #common_name American
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Lund, P.K.; Goodman, R.H.; Montminy, M.R.; Dee, P.C.;
Habener, J.F.

#journal J. Biol. Chem. (1983) 258:3280-3284
#fitle Anglerfish islet pre-proglucagon II. Nucleotide and corresponding amino acid sequence of the cDNA.
#cross-references MUID:83135785
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    #product glucagon-36 (oxyntomodulin) #status
experimental #label G36\/
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                                                                                                                                                          Length 72;
                                                                                                                                                                                                     6; Indels
                                                                                                                                                     Score 119; DB 1; I
Pred. No. 8.84e-07;
10; Mismatches 6;
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##molecule_type protein
##molecule_type protein
1-29;30-60 ##label PLI
                                                                                                            #length 72 #checksum 8055
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Best Local Similarity 44.8%;
Matches 13; Conservative
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A05150
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#title
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REFERENCE
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52-80
89-119
                                                                                                                                                                                                                                                                                                                                                                                        TITLE
CONTAINS
ORGANISM
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                                           1-29
39-70
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TITLE
CONTAINS
1-36
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ENTRY
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CLASSIFICATION #Superfamily glucagon
KEYWORDS
RETWORDS

1-29
#Product glucagon #status experimental #label GCN\
30-60 #Product glucagon-like peptide | #status experimental #label GLI

SUMMARY #length 60 #checksum 8993
Query Match

$0.6%; Score 117; DB 1; Length 60;
Best Local Similarity 41.4%; Pred. No. 1.92e-06;
Matches 12; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
Db 30 HADGIVISNVSTYLODQAAKDFVSWIKSG 58
|::||:||:||:||:||:||:||:||:||:||
Qy | 1 hgegtftsdlskqmeeeavrlffiewlkng 29
Search completed: Mon Oct 4 15:25:57 1999
Job time: 9 secs.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Oct 4 15:24:52 1999; MasPar time 3.93 Seconds 222.856 Million cell updates/sec Run on:

"abular output not generated.

>MOHAM-312-CLAIM82B.PEP (1-31) from moham312177.pep 231 1 hgegtftsdlskqmeeeavrlfiewlknggy 31

Lie: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

77977 seqs, 28268293 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot37 1:swissprot

Mean 35.168; Variance 58.938; scale 0.597 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	1.37e-28	4.69e-27	7.61e-09	2.82e-08	2.82e-08	6.70e-08	1.03e-07	1.59e-07	3.73e-07	3.73e-07	3.73e-07	3.73e-07	3.73e-07	3.73e-07	3.73e-07	3.73e-07	3.73e-07	5.71e-07	5.71e-07	B.72e-07	3.08e-06	7.10e-06	2.45e-05
	Description	EXENDIN-4 PRECURSOR.	•	GLUCAGON PRECURSOR (FR	GLUCAGON-LIKE PEPTIDE	GLUCAGON PRECURSOR (FR	GLUCAGON PRECURSOR (FR	GLUCAGON II PRECURSOR.	GLUCAGON PRECURSOR (FR	GLUCAGON.	GLUCAGON PRECURSOR (FR	GLUCAGON PRECURSOR.	GLUCAGON I PRECURSOR.	GLUCAGON.	GLUCAGON.	GLUCAGON II.								
	a	EXE4_HELSU	EXE3 HELHO	GLUC_RANCA	GLUM_ANGAN	GLUC_ICTPU	GLUC_LEPSP	GLU2_LOPAM	GLUC_ONCKI	GLUC_SCYCA	GLUC_PIG	GLUC_RAT	GLUC_OCTDE	GLUC_MOUSE	GLUC_BOVIN	GLUC_HUMAN	GLUC_CAVPO	GLUC_MESAU	GLUC_CARAU	GLUC_CHICK	GLU1_LOPAM	GLUC_CHIBR	GLUC_TORMA	GLU2_ORENI
	DB	; ;	Н	Н	, –1	Н	Н	М	Н	Н	Н	H	Н	-	Н	Н	٦	П	Н	П	٦	П	Н	Н
	Length	87	39	103	30	71	78	122	68	29	158	180	180	180	180	180	180	180	121	151	124	53	53	33
æ	Query Match	94.8	91.8	53.7	52.4	52.4	51.5	51.1	50.6	49.8	49.8	49.8		49.8	49.8	49.8	49.8	49.8	4.64	49.4		47.6	46.8	45.5
	Score	219	212	124	121	121	119		117	115	115	115	115	115	115	115	115	115	11.4	114	113	110	108	105
	Result	7	7	en	4	Ŋ	9	7	80	6	10	11	12	13	- ≯ :⊣	15	16	17	α	19	20	21	22	23

Query Match 94.8%; Score 219; DB 1; Length 87; Best Local Similarity 100.0%; Pred. No. 1.37e-28;

3.70e-05 3.70e-05 1.87e-04	1.87e-04 2.79e-04 2.79e-04 4.16e-04	9.17e-04 1.36e-03 6.40e-03	2.00e-02 2.00e-02 1.27e-01 2.61e-01	3.73e-01 5.31e-01 5.31e-01 5.31e-01	5.31e-01 5.31e-01 7.53e-01 7.53e-01
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4.52 4.00 6.00	7887 3087	31 33 34	36 35 37	38 440 41	4 4 4 4 2 6 4 7

ALIGNMENTS

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PFAM; PF00123; hormone2; 3. HSSP; P01274; 1GCN.
                                                                                                                                                                                                                                                                  103 AA;
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Best Local Similarity
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TISSUE-PANCREAS;
MEDLINE; 87156787.
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P04093;
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"Purification and structure of exendin-3, a new pancreatic
"Purification and structure of exendin-3, a new pancreatic
J. BIOL. CHEM. 265:20259-20262(1990).
-!- FUNCTION: HAS A VIP/SECRETIN-LIKE BIOLOGICAL ACTIVITY. INTERACTS
-!- FUNCTION: RECEPTOR.
-!- FUNCTION: BELONGS TO THE GLUCAGON FAMILY.
PIR: A23674; HWGH3Z
--- FUNCTION: DELONGS TO THE GLUCAGON FAMILY.
PROSITE; PROOLEGO: GLUCAGON; 1.
PROSITE; PROOLEGO: GLUCAGON; 1.
HSSP; P01274; LGCN.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
NEOBATRACHIA; RANOIDEA; RANIDAE; RANINAE; RANA.
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POLLOCK H.G., HAMILTON J.W., ROUSE J.B., EBNER K.E., RAWITCH A.B.;
"Isolation of peptide hormones from the pancreas of the bullfrog
(Rana catesbelana). Amino acid sequences of pancreatic polypeptide,
J. BIOL. CHEM. 263:9746-9751(1988).
-: FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
THE BLOOD SUGAR LEYEL.
            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-!- X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH OTHER SPECIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       HELODERMA HORRIDUM HORRIDUM (MEXICAN BEADED LIZARD),
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAURIA; SQUAMATA;
SCLEROGLOSSA; ANGUIMORPHA; HELODERMATIDAE; HELODERMA.
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Pred. No. 4.69e-27;
2; Mismatches 0; Indels
            Indels
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                                                                                                                                                                                                                                                                                                01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P15438; P15439; P15440;
01-APK-1990 (REL. 14, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR (FRAGMENTS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLÜCAGON FAMILY; VENOM; AMIDATION.
MOD_RES 39 A9 AMIDATION.
SEQUENCE 39 AA; 4204 MW; AB598FD3 CRC32;
   0; Mismatches
                                                                                                                                                                                                                                                  39 A.A.
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                                                                                          48 HGEGTFTSDLSKQMEEEAVRLFIEWLKNGG 77
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PROSITE; PS00260; GLUCAGON; 3.
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Best Local Similarity 93.3%;
Matches 28; Conservative
Conservative
                                                                                                                                                                                                                                               STANDARD;
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30;
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SEQUENCE.
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MEDINE; 91340068.

CONLON J.M., ANDREWS P.C., THIM L., MOON T.W.;

CONLON J.M., ANDREWS P.C., THIM L., MOON T.W.;

The primary structure of glucagon-like peptide but not insulin has been conserved between the American eel, Anguilla anguilla.";

GEN COMP. ENDOCRINOL. 82:33-32(1991).

-1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

PR.; BEL125; BEL125.

PR.; BEL125; C51125.

PROSITE; PS00126; GLUCAGON; 1.

PRAM; PRO1123; hormone2; 1.

R HSSP; P01374; ANIDATION.

M GLUCAGON FAMILY: AMIDATION.

MOD_RES 30 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANGUILLA ANGUILLA (EUROPEAN FRESHWATER EEL), AND
ANGUILLA ROSTRATA (AMERICAN EEL).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; ANGUILLIFORMES; ANGUILLIDAE; ANGUILLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1986 (REL. 03, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 10, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR (FRAGMENT)
ICTALURUS PUNCTATUS (CHANNEL CATFISH).
EUKARYOTA, METAZOA; CHORDATA, VERTEBRATA; ACTINOPTERIGII; NEOPTERIGII:
TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; SILURIFORMES; ICTALURIDAE;
                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                           Length 103;
                          GLUCAGON.
GLUCAGON-36 (OXYNTOMODULIN).
GLUCAGON-LIKE PEPTIDE 1.
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 30;
                                                                                                                     GLUCAGON-LIKE PEPTIDE 2.
                                                                                                                                                                                      Score 124; DB 1; Le
Pred. No. 7.61e-09;
8; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 121; DB 1; Le
Pred. No. 2.82e-08;
9; Mismatches 6;
                                                                                                                                        D43EDFC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                      | CLUM_ANGAN | STANDARD; | PRT; | 30 AA. |
| P41521; | OLNOV-1995 (REL. 32, CREATED) |
| O1-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) |
| O1-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) |
| GLUCAGON-LIKE PEPTIDE (GLP) |
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27E8C37D CRC32;
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                                                                                                                                                                                                                                                                                                  39 HADGIFISDMSSYLEEKAAKEFVDWLIKG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 HAEGIYISDVSSYLQDQAAKEFVSWLKIG 29
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36 GL
70 GL
71
1103 GL
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                                                                                                                                                                               Query Match 53.7%;
Best Local Similarity 51.7%;
Matches 15; Conservative
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ilarity 48.3%;
Conservative
GLUCAGON FAMILY; HORMONE
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ANDREWS P.C., RONNER P.;

"Isolation and structures of glucagon and glucagon-like peptide from cattish pancreas.";

"Isolation and structures of glucagon and glucagon-like peptide from cattish pancreas.";

"J. BICL. CHEM. 260:3910-3914(1985).

"I. FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES C. THE BLOOD SUGAR LEVEL.

"I. INDUCTION: PROMOTED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

"I. X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH AMERICAN GOOSFEISH SEQUENCES.

"INTLARITY: BELONGS TO THE GLUCAGON FAMILY.

R PIR, AOSIFIE; PSOUGO, GLUCAGON, 2.

R PERM: PROSITE; PSOUGO, GLUCAGON, 2.
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LEPISOSTEUS SPATULA (ALLIGATOR GAR) (ATRACTOSTEUS SPATULA).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII; SEMIONOTIFORMES; LEPISOSTEIDAE; LEPISOSTEUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insulin and pancreatic polypeptide.";
GEN. COMP. ENDOCRINOL. 67:375-382(1987).
-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS. AND RAISES
THE BLOOD SUGAR LEVEL.
-!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
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LANCE V., RAWITCH A.B.;
Isolation of alligator gar (Lepisosteus spatula) glucagon, oxyntomodulin, and glucagon-like peptide: amino acid sequences of oxyntomodulin and glucagon-like peptide.";
GEN. COMP. ENDOCRINOL. 69:133-140(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLLOCK H.G., KIMMEL J.R., HAMILTON J.W., ROUSE J.B., EBNER K.E., LANCE V., RAWITCH A.B.;
"Isolation and structures of alligator gar (Lepisosteus spatula)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
HOOSEIN N.M., MAHRENHOLZ A.M., ANDREWS P.C., GURD R.S.; "Biological activities of catfish glucagon and glucagon-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLUCAGON-LIKE PEPTIDE,
E -> D (IN REF. 2).
                                                   SIOCHEM. BIOPHYS. RES. COMMUN. 143:87-92(1987)
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1095567 (REL. 10, CREATED) 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE) 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C49ED93A CRC32;
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8173 MW;
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Best Local Similarity 51.7%;
Matches 15; Conservative
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                                                                                                                          MEDLINE; 85157536.
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                                                                                                         IISSUE-PANCREAS;
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01-NOY-1986 (REL. 03, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUCAGON II PRECURSON.
LOPHIUS AMBRICANUS (AMERICAN GOOSEFISH) (ANGLERFISH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PARACANTHOPTERYGII; LOPHIIFORMES; LOPHIIDAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 86286913.

NOE B.D., ANDREWS P.C.;

"Specific glucagon-related peptides isolated from anglerfish islets are metabolic cleavage products of (pre)proglucagon-II.";

PEPTIDES 7:331-339(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LUND P.K., GOODMAN R.H., MONTMINY M.R., DEE P.C., HABENER J.F.; "Anglerfish islet pre-proglucagon II. Nucleotide and corresponding amino acid sequence of the CDNA."; J. BIOL. CHEM. 258:3280-3284(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE BLOOD SUGAR LEVEL.
-!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-!- SIMILARITY: BELONGS TO THE GLOCAGON FAMILY.
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-!- X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH AMERICAN
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                                                                                                                                                                                                                                                                             GLUCAGON-36 (OXYNTOMODULIN).
GLUCAGON-LIKE PEPTIDE.
509ED9D3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                Score 119; DB 1; Length 78;
Pred. No. 6.70e-08;
10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLUCAGON II.
GLUCAGON-LIKE PEPTIDE II.
; DFE63061 CRC32;
                            GOOSEFISH SEQUENCES.
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
PIR; S06339; GCGXA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 AA.
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                                                                                                                                                                                                                                                    GLUCAGON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; V00632; G64022; -.
EMBL; V00933; G213353; -.
PIR; A05150; GGAP.
PROSITE; PS00260; GLUCAGON; 2.
PFAM; PF00123; hormone2; 2.
HSSP; P0174; 1GCN.
GLUCAGON FAMILY; HORMONE; CLEAVA
                                                                                                                  PROSITE; PS00260; GLUCAGON; 2.
PFAM; PF00123; hormone2; 2.
HSSP; P01274; IGCN.
GLUCAGON FAMILY; HORMONE.
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                                                                                                                                                                                                                                                                                                                                   78 AA; 8990 MW;
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Best Local Similarity 44.8%;
Matches 13; Conservative
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AC 01-NOV-1986

DT 01-NOV-1986

DT 01-NOV-1986

DE GLUCAGON II

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RY MEDLINE; 81

RY MEDLINE; 81

RY MEDLINE; 862

RY MEDLINE; 763

CC -1- FUNCTION

CC -1- FUNCTION

CC -1- INDUCTION

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                                                                                                                                                                                                                                                             GLUCAGON PRECURSOR (FRAGMENT).
ONCORHYNCHUS KISUTCH (COHO SALMON).
EUKARYOTA: METALOA: CHORDATA: VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII; TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES;
                                                                                                                                                                                                                                                                                                                                                                                MEDIINE; 86234328.
PLISETSKAYA E., POLLOCK H.G., ROUSE J.B., HAMILTON J.W., KIMMEL J.R.,
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCYLIORHINUS CANICULA (SPOTTED DOGFISH) (SPOTTED CATSHARK).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; CHONDRICHTHYES;
ELASMOBRANCHII; CARCHARHINIFORMES; SCYLIORHINIDAE; SCYLIORHINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolation and structures of coho salmon (Oncorhynchus kisutch)
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          Score 118; DB 1; Length 122;
Pred. No. 1.03e-07;
10; Mismatches 6; Indels
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Pred. No. 1.59e-07;
12; Mismatches 5; Indels
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                                                                                                                                                                                                          01-APR-1988 (REL. 07, CREATED)
01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-JAN-1990 (REL. 13, LAST ANNOTATION UPDATE)
                                                                                                                                                                                   68 AA.
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                                                                             89 HADGTYISDVSSYLQDQAAKDFVSWLKAG 117
                                                                                               38 HADGIYISNVSIYLQDQAAKDFVSWLKSG 66
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MEDLINE; 87190953.
CONLON J.M., O'TOOLE L., THIM L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68
7810 MW;
       Query Match
Best Local Similarity 44.8%;
Matches 13; Conservative
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ilarity 41.4%;
Conservative
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SALMONIDAE; ONCORHYNCHUS.
                                                                                                                                                                                 STANDARD;
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Matches 12; Conser
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68 AA;
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P09687;
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SEQUENCE
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"Primary structure of glucagon from the gut of the common dogfish (Scyliothinus canicula)."
FEBS LETT. 214:50-56(1987).
FEBS LETT. 214:50-56(1987).
ITE BLOOD SUGAR HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEE.
-1- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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MEDLINE; 88243712.
BUHL T., THIM L., KOFOD H., ORSKOV C., HARLING H., HOLST J.J.,
"Naturally occurring products of proglucagon 111-160 in the porcine
and human small intestine.";
J. BIOL. CHEM. 263:8621-8624(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 76051297.
SASAKI K., DOCKERILL S., ADAMIAK D.A., TICKLE I.J., BLUNDELL T.L.;
"X-ray analysis of glucagon and its relationship to receptor binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECURINCE OF 33-61.
BROWER W.W., SINN L.G., BEHRENS O.K.;
The amino acid sequence of glucagon. V. Location of amide groups,
acid degradation studies and summary of sequential evidence.";
J. AM. CHEM. SOC. 79:2807-2810(1957).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 78-107.
MEDLINE; 89327238.
ORSKOV C., BERSANI M., JOHNSEN A.H., HOEJRUP P., HOLST J.J.;
"Complete sequences of glucagon-like peptide-1 from human and pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERLA; ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THIM L., MOODY A.J.; "The primary structure of porcine glicentin (proglucagon)."; REGUL. PEPT. 2:139-150(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 115; DB 1; Length 29;
Pred. No. 3.73e-07;
7; Mismatches 6; Indels
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MEDILINE; 82221776.
THIM L., MOODY A.J.;
"THE amino acid sequence of porcine glicentin.";
PEPTIDES 2 SUPPL. 2:37-39(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (REL. 01, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                      SCFE41FB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 AA
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| hgegtftsdlskqmeeeavrlfiewlkn 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                    PIR, A26992, GCDF.
PROSITES, PSO10260, GLUCAGON; 1.
PFAM; PF00123; hormone2; 1.
HSSP; P01274; 1GCN.
                                                                                                                                                                                                                                                                                                                                                                                   29 AA; 3529 MW;
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MEDLINE; 81248172.
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MOHAM-312-CLAIM82B.PEP.rsp

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PFAM; PF00123; hormone2; 3.
HSSP; P01274; IGCN.
                                                                                                                                                                                                                                                                                                                                                      EMBL; K02809; G204370; JOINED.
EMBL; K02810; G204370; JOINED.
EMBL; K02811; G204370; JOINED.
EMBL; K02812; G204370; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.2%;
Matches 16; Conservative
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PIR; A44198; A44198.
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P22890;
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SEQUENCE
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PEPTIDE
PEPTIDE
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              SO THE PRESENTATION OF THE
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HEIMRICH G., GROS P., HABENER J.F.;
"Glucagon gene sequence. Four of six exons encode separate functional domains of rat pre-proglucagon.";
J. BIOL. CHEM. 259:14082-14087(1984).
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"EVECTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.

"I HE BLOOD SUGAR LEVEL.

"I HE SPOUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

"I RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

"I RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-!- STMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLICENTINE RELATED POLYPEPTIDE)
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00123; hormone2; 3. GLUCAGON FAIR OF BASIC RESIDUES; GLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 85051023.
HEINRICH G., GROS P., LUND P.K., BENTLEY R.C., HABENER J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEĞUENCE FROM N.A.
MEDLINE, 86304324.
MOJSOV S., HEINRICH G., WILSON I.B., RAVAZZOLA M., ORCI L.,
HABENER J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 115; DB 1; Length 158;
Pred. No. 3.73e-07;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLUCAGON-LIKE PEPTIDE 1. GLUCAGON-LIKE PEPTIDE 2.
                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
PIR; A01540; GCPG.
PDB; 1GCN; 30-SEP-83.
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18212 MW; 9FBC1BFE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 AA.
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GLUCAGON.
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ENDOCRINOLOGY 115:2176-2181(1984).
                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00260; GLUCAGON; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.2%;
Matches 16; Conservative
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107
107
158
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GLUC_RAT
P06883;
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PEPTIDE
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PFAM; PF00123; hormone2; 3.
HSSP; P01274; IGCN.
GLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NISHI M., STEINER D.F.;
"Cloning of complementary DNAs encoding islet amyloid polypeptide,
"Cloning of complementary DNAs encoding islet amyloid polypeptide,
insulin, and glucagon precursors from a New World rodent, the degu,
octodon degus.",
MOL. ENDOCRINOL. 4:1192-1198(1990).
-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
THE BLOOD SUGAR LEVER LEVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 115; DB 1; Length 180; Pred. No. 3.73e-07; 6; Mismatches 7; Indels
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GLUCAGON-LIKE PEPTIDE 1.
GLUCAGON-LIKE PEPTIDE 2.
; 355C3843 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
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180 AA

PRT;

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCDONALD J.K., MACKIN R.B., NOE B.D.;
"Processing of mouse proglucagon by recombinant prohormone convertase 1 and immunopurified prohormone convertase 2 in vitro.";
J. BIOL. CHEM. 270:10136-10146(1995).
-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.
 CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL. SIGNAL 1 20 BY SIMILARITY.
                                                                                                                                                                                Gaps
                                                        GLUCAGON.

GLUCAGON-LIKE PEPTIDE 1.

GLUCAGON-LIKE PEPTIDE 2.

AMIDATION (G-128 PROVIDE AMIDE GROUP).

4AlF5CE3 CRC32;
                                            GRPP (GLICENTINE RELATED POLYPEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLYPEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROTHENBERG M.E., EILERTSON C.D., KLEIN K., ZHOU Y., LINBERG I.
                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                             GCG.
MUS MUSCULUS (MOUSE).
EUKARXOIA: METAZOA; CHORDAIA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                             Score 115; DB 1; Length 180;
Pred. No. 3.73e-07;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 115; DB 1; Length 180;
Pred. No. 3.73e-07;
6; Mismatches 7; Indels
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GLUCAGON-LIKE PEPTIDE 2.
0B21B7BA CRC32;
                                                                                                                                                                                                                                                                        LT 13
GLUC_MOUSE STANDARD; PRT; 180 AA.
610C_MOUSE STANDARD; PRT; 180 AA.
01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0UL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR.
                                                                                                                                                                                                    98 HAEGTFISDVSSYLEGQAAKEFIAWLVKG 126
                                                                                                                                                                                                                       GRPP (GLI GLU GLUCAGON.
                           20 BY
50 GR
81 GL
128 GL
178 GL
20906 MW;
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PROSITE: PSOD260; GLUCAGON; 4.
PFAM; PF00123; hormone2; 3.
HSSP; P01274; LGCN.
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                                                                                                                                             Ouery Match 49.8%;
Best Local Similarity 55.2%;
Matches 16; Conservative
 FAMILY; HORMONE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-PANCREATIC ISLETS;
MEDLINE; 95247722.
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53
92 1
146 1
127 1
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                         BROWER W., BOUCHER M.E., KOFFENBERGER J.E. JR.;
"Anino acid sequence of bovine glucagon.";
J. BIOL. CHEM. 246:2822-2827(1971).
-1- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
THE BLOOD SUGAR LEVEL.
                                                                                                                                                                                                                       LOPEZ L.C., FRAZIER M.L., SU C.-J., KUMAR A., SAUNDERS G.F., "Mammalian pancreatic preproglucagon contains three glucagon-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                   -1- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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                                                                                                                                BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 115; DB 1; Length 180;
Pred. No. 3.73e-07;
6; Mismatches 7; Indels
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GLUCAGON-LIKE PEPTIDE 2.
T -> Y (IN PIR DATA BANK).
34640341 CRC32;
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                                                       21-JUL-1986 (REL. 01, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (REL. 01, CREATED)
13-AGG-1987 (REL. 05, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR.
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81 GI
128 GI
178 GI
157 T
20944 MW;
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157
180 AA;
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nes 16; Conserv
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MEDLINE: 71166445.
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14
GLUC_BOVIN
P01272;
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GLUC_HUMAN
P01275;
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CONFLICT
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Search completed: Mon Oct 4 15:24:58 1999 Job time: 6 secs.
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ORSKOV C., BERSANI M., JOHNSEN A.H., HOEJRUP P., HOLST J.J.;
"Complete sequences of glucagon-like peptide-1 from human and pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLUCAGON-LIKE PEPTIDE 1. GLUCAGON-LIKE PEPTIDE 2.
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THOMSEN J., KRISTIANSEN K., BRUNFELDT K., SUNDBY F.;
"The amino acid sequence of human glucagon.";
FEBS LETT. 21:315-319(1972).
                                                                            MEDLINE; 88330860.
DRUCKER D.J., ASA S.;
"Glucagon gene expression in vertebrate brain.";
J. BIOL. CHEM. 263:13475-13478(1988).
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                                                                                                                                                                                                                                  MEDLINE; 86259053.
WHITE J.W., SAUNDERS G.F.;
"Structure of the human glucagon gene.";
NOCLEIC ACIDS RES. 14:4719-4730(1986).
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  small intestine.";
J. BIOL. CHEM. 264:12826-12829(1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J04040; G183270; -. EMBL; X03991; G762941; -. EMBL; V01515; G31778; -.
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PIR; S23309; S23309.
MIM; 138030; -.
MIM; 231530; -.
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                                                          Query Match 49.8%; Score 115; DB 1; Length 180; Best Local Similarity 55.2%; Pred. No. 3.73e-07; Matches 16; Conservative 6; Mismatches 7; Indels
82 K -> N (IN REF. 3).
20909 MW; DEE43985 CRC32;
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Oct 4 15:25:15 1999; MasPar time 10.69 Seconds 158.226 Million cell updates/sec Run on:

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>MOHAM-312-CLAIM82B.PEP (1-31) from moham312177.pep 231 1 hgegtftsdlskqmeeeavrlfiewlknggy 31 rtle:
Description:
Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_bhage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 33.531; Variance 62.579; scale 0.536 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SITMMARTES

	Pred. No.		3.34E-17	3.51e-11	4.25e-07	4.25e-07	4.25e-07	4.25e-07	4.25e-07	4.51e-06	4.58e-05	4.58e-05	5.81e-03	1.40e-01	7.64e-01	2.06e+00	2.85e+00	2.85e+00	3.93e+00	3.93e+00	3.93e+00	3.93e+00	
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XENOPUS LAEVIS (AFRICAN CLAWED FROG). EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.

[1] SEQUENCE FROM N.A.

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C6.1A. INTEGRASE/RECOMBINASE. 172589.7 PROTEIN. ADENYLYL-SULPHATE REDU PEPTIDYLARGININE DEIMI FORMATE DEHYDROGENASE VOLTAGE-GATED CALCIUM HOMOPROTOCATECHUATE DY HYPOTHETICAL 61.6 KD P DINYDROGEODIN OXIDASE. CARBOXYEPTIDASE. MICROFILARIAL GHITINAS MICROFILARIAL CHITINAS MITRITER REDUCTASE (EC 1352AA LONG HYPOTHETIC ESTERASE. INTERMEDIATE FILAMENT KIANO318 (FRAGMENT) UDP-GLUCOSE DEHYDROGEN NADH DEHYDROGENASE SUB
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ALIGNMENTS

1998 (TREMBLREL. 05, CREATED) 1998 (TREMBLREL. 05, LAST SECU- 1998 (TREMBLREL. 05, LAST SECU- 1998 (TREMBLREL. 06, LAST ANNO AGON I. LAEVIS (ARRICAN CLAWED FROG). 18, METAZOA; CHORDATA; VERTEBR- ACHIA; PIPOIDEA; PIPIDAE; XEN 197388292. 197388292. 19738292. 19738292. M. SATKUNARAJAH M., WEN Y., M.B.; SATKUNARAJAH M., WEN Y., M.B.; ALTKUNARAJAH M., WEN Y., M.B.; SATKUNARAJAH M., WEN Y., 1011 1 1 1 1 1 1 1 1 1	ID OI	042143	PRELIMINARY;	PRT;	266 AA.
01-70x-1998 (TREMELREL. 05, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMELREL. 08, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE) PROGLUCAGON I XENOPUS LAEVIS (AFRICAN CLAWED FROG) EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; MESOBATRACHIA: PIPOIDEA: PIPIDAE; XENOPODINAE; XENOPUS. [1] SEQUENCE FROM N.A. MEDLINE: 97388292 IRMIN D.M.; SATKUNRAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A., WHEELER M.B.; "THA EXHOPUS DIOJUCAGON GENE encodes novel GLP-1-like peptides with insulinotropic properties."; PROG. NATL. ACAD. SCI. US.A. 94:7915-7920(1997). PROG. NATL. ACAD. SCI. US.A. 94:7915-7920(1997). PROSITE: PS00260; GLUCAGON; 5. PROSITE: PS00260; GLU	AC.	042143;			
01-NOV-1998 (TREMELREL. 05, LAST SEQUENCE UPDATE) PROGUCAGON I. XENOPUS LAEVIS (AFRICAN CLAMED FROG). EUKRYOTA, WETAZOA; CHORDATA; VERTEBRATA; MAPHIBIA; BATRACHIA; ANURA; MESCBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS. [1] SEQUENCE FROM N.A. MEDLINE; 97386292. IRWIN D.M., SATKUNARAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A., WHEEDER M.B.; The Xenopus properties."; "The Xenopus properties."; "The Xenopus properties."; PROG. NATL. AAAD. SCI. U.S.A. 94:7915-7920(1997). EMBE; AROO4422; G3305016; D. PROSITE; PS00260; GLUCAGON; S. PFAM; PF00123; hormone2; S. SEQUENCE 266 AA; 30951 MW; E6139A25 CRC32; SEQUENCE 1000 SIMILATITY 60.0%; Pred. No. 9.94e-12; MATCHES 18; CONSETVATIONE 7; Mismatches 5; Indels 0; Gaps 97 HARGTESDYTOQLEKAAKEFIDWLING 126 : : :	ΔŢ	01-JAN-1998			
Ol-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) PROGLUCAGON I. XENOPUS LAEVIS (AFRICAN CLAWED FROG). EUKARYOTA, WETAZOA; CHORDATA; VERTEBRATA; AMPHIBIA: BATRACHIA; ANURA; MESOBATRACHIA: PIPOIDEA: PIPIDAE; XENOPODINAE; XENOPUS. [1] SEQUENCE FROM N.A. MEDLINE; 97368292. IRWIN D.M., SATKUNARAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A., WHEELER M.B.; "The Xenopus proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties."; PROC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997). EMBL; AFO04422; G2305016; PROSITE; PS00260; G1UCAGON; 5. PFAM: PF00123; hormone2; 5. SEQUENCE 266 AA; 30951 MM; E6139A25 CRC32; SEQUENCE 266 AA; 30951 MM; E6139A25 CRC32; SUBJETA MATCH 60.0%; PIPICA. NO. 9.94e-12; MATCHES 18; CONSELVATIVE 7; Mismatches 5; Indels 0; Gaps 97 HAEGTETSDYTOQLDERAAKEFIDMLINGG 126	텀	01-JAN-1998			(UENCE UPDATE)
PROGLUCAGON I. **RENORUS LAEVIS (AFRICAN CLAMED FROG).** **EUNARYCTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; BUKARYCTA; METAZOA; CHORDATA; VERTEBRATA; XENOPUS. [1] SEQUENCE FROM N.A. **RESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS. [2] SEQUENCE FROM N.A. **MEDILINE; 97368292.** IRWIN D.M.; SATKUNARAJAH M.; WEN Y.; BRUBAKER P.L.; PEDERSON R.A.; WHEELER M.B.; THA KAROPUS PYCOGLOGON Gene encodes novel GLP-1-like peptides with insulinotropic properties.; ** **The Kanopus Pycoglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties.; ** **PROG. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997).** **PROSITE; PSO0260; GLUCAGON; 5.* **PROSITE; PSO0260; GLUCAGON; 7.* **MATCHAGON; PRELIMINARY; PRT; 219 AA. O42144; O1-JAN-1998 (TREMBLREL. O5, LAST SEQUENCE UPDATE) O1-JAN-1998 (TREMBLREL. O6, LAST SEQUENCE UPDATE) PROGLUCAGON II. **PROSITE PRELIMINARY OF TARBELREL. O6, LAST SEQUENCE UPDATE) O1-NAV-1998 (TREMBLREL. O6, LAST SEQUENCE UPDATE) PROGLUCAGON II.	텀	01-NOV-1998			OTATION UPDATE)
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; MESOBATRACHIA; PIPOIDEA; PIPOIDEA; PIPOIDEA; PIPOIDEA; PIPOIDEA; PIPOIDEA; ENOPOUNAE; XENOPUS. [1] SEQUENCE FROM N.A. MEDILINE; 97368292 IRWIN D.M.; SATKUNARAJAH M.; WEN Y.; BRUBAKER P.L.; PEDERSON R.A.; WHEELIER M.B.; "The Xenopus proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties."; "The Xenopus proglucagon gene encodes novel GLP-1-like peptides with PROC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997). EMBL; AFOON4432; G2305016; PROS. TEXT. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997). EMBL; AFOO123; hormone2; 5. SEQUENCE 266 AA; 30951 MW; E6139A25 CRC32; SEQUENCE 266 AA; 30951 MW; E6139A25 CRC32; ACAD. SIMILATITY 60.0%; Pred. No. 9:94e-12; MATCHES 18; CONSERVATIVE 7; Mismatches 5; Indels 0; Gaps 97 HAEGTFTSDVTQQLDEKAAKEFIDWINGG 126	DE	PROGLUCAGON	H.		
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS. [1] SEQUENCE FROM N.A. MEDLINE; 9736829. IRWIN D.M., SATKUNARAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A., WHEBLER M.B.; PROPERTIES."; PROC. NATL, ACAD. SCI. U.S.A. 94:7915-7920(1997). EMBL; AFO04422; G2305016; PROSITE; PS00260; G1UCAGOU; 5. PRAM; PF00123; hormone2; 5. SEQUENCE 266 AA; 30951 MM; E6139A25 CRC32; SUGURCE 266 AA; 30951 MM; E6139A25 CRC32; SUGURCE 266 AA; 30951 MM; E6139A25 CRC32; SUGURCE 266 AA; 30951 MM; E11940; BB 13; Length 266; Best Local Similarity 60.0%; Pred. No. 9.94e-12; MATCHES 18; CONSELVATIVE 7; Mismatches 5; Indels 0; Gaps 97 HAEGTFFTSDVTQQLDEKAAKEFTDMLINGG 126	SO	XENOPUS LAEV	IS (AFRICAN CL.	AWED FROG)	•
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPOINAE; XENOPUS. SEQUENCE FROM N.A. MEDILINE; 97368292 IRWIN D.M.; SATKUNARAJAH M.; WEN Y.; BRUBAKER P.L.; PEDERSON R.A.; WHEELER M.B.; SATKUNARAJAH M.; WEN Y.; BRUBAKER P.L.; PEDERSON R.A.; WHEELER M.B.; The Xenopus proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties.; 94:7915-7920(1997). PROSITE; PSO0260; GLUCAGON; 5. PROSITE; PSO0260; GLUCAGON; 5. PRAMI, PRO0123; hornone2; 5. 5. PROSITE; PSO0260; GLUCAGON; 5. PROSITE; PSO0260; GLUCAGON; 5. PROSITE; PSO0260; GLUCAGON; 5. PROSITE; PSO0260; GLUCAGON; 63:2%; SCOTE 146; DB 13; Length 266; PROSITE; PSOUDOREXAKEFIDWLINGG 126 1:	8	EUKARYOTA; M	ETAZOA; CHORDA	ra; Verteb	ATA; AMPHIBIA; BATRACHIA;
SEQUENCE FROM N.A. MEDLINE: 97368292 IRWIN D.M., SATKUNARAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A., WHEELINE M.B.; "The Xenopus proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties."; PROCUED TO WATL. ACAD. SCI. U.S.A. 94:7915-7920(1997). EMBL; AFO04432; G2305016; PROSITE; PS00260; GLUCAGON; 5. PROM; PF00123; hormone2; 5. SEQUENCE 266 AA; 30951 MW; E6139A25 CRC32; SEQUENCE 266 AA; 30951 MW; E6139A25 CRC32; ACATUATO CONSERVATIVE NO. 9.94e-12; MATCHES 18; CONSERVATIVE NO. 9.94e-12; MATC	8	MESOBATRACHI	A; PIPOIDEA; P.	IPIDAE: XE	NOPODINAE: XENOPUS.
SEQUENCE FROM N.A. MEDLINE; 97368292. IRWIN D.M., SATKUNARAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A., WHEBLER M.B.; PROPULS 97368292. IRWIN D.M., SATKUNARAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A., WHEBLER M.B.; proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties."; PROPULS; proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties."; PROC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997). EMBL; AFO04423; G2305016; PROCIECAGO; FRAM; PRO0123; hormone2; 5. SEQUENCE 266 AA; 30951 kM; E6139A25 CRC32; SEQUENCE 266 AA; 30951 kM; E6139A25 CRC32; SEQUENCE 266 AA; 30951 kM; E6139A25 CRC32; SEQUENCE SIB; Conservative 7; Mismatches 5; Indels 0; Gaps 97 HAEGTETSDVTQQLDEKAAKEFIDMLINGG 126	RN	Ξ			
MEDLINE; 97368292. IRMIN D.M., SATKUNARAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A., WHEBLER M.B.; WHEBLER M.B.; "The Xanopus proglucaging gene encodes novel GLP-1-like peptides with insulinotropic properties."; PROC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997). PROSITE; PS00260; GLUCAGON; S. PRAMI: PF004423; G205016;	RP	SEQUENCE FRO	M N.A.		
IRWIN D.M., SATKUNARAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A., WHERLENE M.B.; "The Xenopus proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties."; PROC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997). EMBL; AF004432; G2305016; PROSITE; PS00260; GLUCAGON; 5. PROMIT PRO123; hormone2; 5. SEQUENCE 266 AA; 30951 MW; E6139A25 CRC32; SEQUENCE 266 AA; 30951 MW; E6139A25 CRC32; SEQUENCE 266 AA; 30951 MW; E6139A25 CRC32; MATCHA 63.2%; SCORE 146; DB 13; Length 266; Best Local Similarity 60.0%; Pred. No. 9.94e-12; MATCHA 60.0%; Pred. No. 9.94e-12; MATCHA 1996 CONSERVATIVE 7; MISMATCHES 5; Indels 0; Gaps 97 HAEGTFTSDVTQQLDERAAKEFIDWINGG 126	RX	MEDLINE; 973	168292.		
WHEBLER M.B.; "The Kanopus proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties."; PROC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997). EMBL; AF004432; G230516; PROSITE; PS00260; G1UCAGON; 5. SEQUENCE 266 AA; 30951 MM; E6139A25 CRC32; SUGENCE 266 AA; 30951 MM; E613PA2E CRC32; SUGENCE 266 AA; 30951 MM; EAST ANNOTATION UPDATE) PROGLUCAGON II.	æ	IRWIN D.M.	SATKUNARAJAH M	., WEN Y.,	BRUBAKER P.L., PEDERSON R.A.,
"The Xenopus proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties."; PROC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997). EMBL; AF004432; G2305016;	æ	WHEELER M.B.	•••		
insulinotropic properties.; PROC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997). EMBL; AFO04432; G2305016; PROSITE; PS00260; GLUCAGON; 5. PRAM; PF00123; hormone2; 5. SEQUENCE 266 AA; 30951 MW; E6139A25 CRC32; SEQUENCE 266 AA; 30951 MW; E6139A25 CRC32; SEQUENCE 266 AA; 30951 MW; E6139A25 CRC32; MATCH 63.2%; Score 146; DB 13; Length 266; Best Local Similarity 60.0%; Pred. No. 9.94e-12; MATCHES 18; CONSERVATIVE 7; Mismatches 5; Indels 0; Gaps 97 HAEGTFTSDVTQQLDEKAAKEFIDWLING 126	RI	"The Xenopus	prodlucadon de		s novel GLP-1-like peptides with
PROC. NATL ACAD. SCI U.S.A. 94:7915-7920(1997). EMBL; AF004432; G2305016; PROSITE; PS00260; G1UCAGON; 5. FRAM; PF00123; hormone2; 5. SEQUENCE 26 AA; 30951 MW; E6139A25 CRC32; SUCTION Similarity 60.0%; Pred. No. 9.94e-12; MATCHES 18; CONSELVATIVE 7; Mismatches 5; Indels 0; Gaps 97 HAGGFFTSDVTQQLDEKAAKEFTDWLINGG 126 : :: :	RI	insulinotrop	of properties.		
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PROSITE; PS00260; GLUCAGON; 5. PROSITE; PS00260; GLUCAGON; 5. PFRAM; PF00123; hormone2; 5. SEQUENCE 266 AA; 30951 MW; E6139A25 CRC32; Duery Match 63.2%; Score 146; DB 13; Length 266; Matches 18; Conservative 7; Mismatches 5; Indels 0; Gaps 97 HAEGTFTSDVTQQLDEKAAKEFLDWLINGG 126 : : : : :	DR	EMBL: AF0044	32: G2305016:		
PFAM; PF00123; hormone2; 5. SEQUENCE 26 AA; 30951 MW; E6139A25 CRC32; Duery Match 63.2%; Score 146; DB 13; Length 266; Best Local Similarity 60.0%; Pred. No. 9.94e-12; Matches 18; Conservative 7; Mismatches 5; Indels 0; Gaps 97 HAEGTPTSDVTQQLDEKAAKEFIDMLINGG 126 : :: :	DR	PROSITE; PS0		, N	
SEQUENCE 266 AA; 30951 MW; E6139A25 CRC32; Duery Match 63.2%; Score 146; DB 13; Length 266; Best Local Similarity 60.0%; Pred. No. 9.94e-12; Matches 18; Conservative 7; Mismatches 5; Indels 0; Gaps 97 HAEGTFTSDVTOQLDEKAAKEFIDWLINGG 126 : :: :: : :	DR	PFAM; PF0012	3; hormone2; 5		
Duery Match 63.2%; Score 146; DB 13; Length 266; Best Local Similarity 60.0%; Pred. No. 9.94e-12; Matches 18; Conservative 7; Mismatches 5; Indels 0; Gaps 97 HAEGTFTSDVTQQLDEKAAKEFIDWLINGG 126 : :: : :	SO	SEQUENCE 2	66 AA; 30951 1	 	A25 CRC32;
Best Local Similarity 60.0%; Pred. No. 9.94e-12; Matches 18; Conservative 7; Mismatches 5; Indels 0; Gaps 97 HAEGTFTSDVTQQLDEKAAKEFIDWLING 126 : :: : :	ð	ery Match	63.28;	Score 14	
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ONCORHYNCHUS MYKISS (RAINBOW TROUT) (SALMO GAIRDNERI).
EUKARYOIA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSIEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
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"Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
MACL. ENDOCRINOL. 9:267-277(1995).
EMBL; U19913; G736361;
PFRM; PF00123; hormone2; 2.
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"Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
MOL. ENDOCRINOL. 9:267-277(1995).
EMBL: S78474; E206590; -.
MEDLINE; 97368292.
IRWIN D.M., SATKUNARAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A., WHEELER M.B.;
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Pred. No. 3.51e-11;
8; Mismatches 5; Indels
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
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Pred. No. 4.25e-07;
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Best Local Similarity 56.7%;
Matches 17; Conservative
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44.8%;
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les 13; Conservative
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MEDLINE; 95295739.
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MEDLINE, 95295739.
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BURARYOTA: METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
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01-NOY-1996 (TREMBLREL. 01, CREATED)
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01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOY-1998 (TREMBLREL. 08, CATINOTATION ENGINERY ON EURARYOTA, METAZOA, CHORDARA, VERTEBRATA, ACTINOPIERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDILINE; 95295739.
ITRNIN D.M., WONG J.;
"Irout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
EMBL; 878473; 6999383;
PRAM; PF00123; hormone2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRWIN D.M., WONG J.;
"Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
MOL. ENDOCRINOL. 9:267-277(1995).
EMBL; S78475; G999385; -.
PROSITE; PS00260; GUCAGON; 3.
PPRAM; PF00123; hormone2; 3.
SEQUENCE 178 AA; 20034 MW; 2056F963 CRC32;
                                                                                                 ;
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                                                      Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 72;
                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 120; DB 13; Length 72
Pred. No. 4.25e-07;
11; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                               LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                 Score 120; DB 13; I
Pred. No. 4.25e-07;
11; Mismatches 5;
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Pred. No. 4.25e-07;
       OF7AF3EC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF7AF3EC CRC32;
                                                                                                                                                                                                                                                                             72
                                                                                                                                                                39 HADGIYISDVSIYLQDQAAKDFVSWLKSG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 HADGIYISDVSIYLQDQAAKDFVSWLKSG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 hgegtftsdlskgmeeeavrlfiewlkng 29
                                                                                                                                                                                                                                                                                                                          CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECTENCE FROM N.A.
TISSUE-INTESTINE, DISTAL PORTION;
MEDLINE; 95295739.
                                                                                                                                                                                                                                                                                                                        01,
08,
72 AA; 8293 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 AA; 8293 MW;
                                            Query Match 51.9%;
Best Local Similarity 44.8%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 51.9%;
Best Local Similarity 44.8%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.9%;
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921408
921408;
031408;
01-NOV-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. O
01-NOV-1998 (TREMBLREL. O
PROGLUCAGON (FRAGMENT).
                                                                                                                                                                                                                                                                           PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ONCORHYNCHUS.
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NON_TER
SEQUENCE
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MOHAM-312-CLAIM82B.PEP.rspt

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Matches

RESULT
099
DT 001
DD 01

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RABIES VIRUS.
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES; RHABDOVIRIDAE;
LYSSAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HELODERMA SUSPECTUM (GILA MONSTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAURIA; SQUAMATA;
SCLEROGLOSSA; ANGUIMORPHA; HELODERMATIDAE; HELODERMA.
                                                                                                                             HELODERMA SUSPECTUM (GILA MONSTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAURIA; SQUAMATA;
SCLEROGLOSSA; ANGUIMORPHA; HELODERWATIDAE; HELODERMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 204;
                                                                                                                                                                                                                                                                                                                                Length 149;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                              04, CREATED)
04, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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01-070-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-070-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
1 PROTEIN, RNA DEPENDENT RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                           / Match 46.8%; Score 108; DB 13; I
Local Similarity 48.3%; Pred. No. 4.58e-05;
nes 14; Conservative 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
46.8%; Score 108; DB 13; I
Best Local Similarity 48.3%; Pred. No. 4.58e-05;
Matches 14; Conservative 7; Mismatches 8;
                                                                                                                                                                                           CHEN Y.E., DRUCKER D.J.;
J. BICL. CHEM. 0:0-0/0(0).

EMBL, U77611; 61916063; -.

PRAM; PF00123; hormone2; 2.

SEQUENCE 149 AA; 17224 MW; F763AB51 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
CHEN Y.E., DRUCKER D.J.;
L. BLOL. CHEN. 0.0-0(0).
EMBL; U77612; G1916065; -.
PROSITE; PS00260; GLUCAGOO.
PROSITE; PS00123; hormone2; SEQUENCE 204 AA; 23553 MW; EE50250D CRC32;
                  149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 HADGRYTSDISSYLEGQAAKEFIAWLVNG 144
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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08,
08,
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012956, 012956;
01-JUL-1997 (TREMBLREL. 0.
01-JUL-1997 (TREMBLREL. 0.
01-NOV-1998 (TREMBLREL. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                 PRELIMINARY;
                                              01-JUL-1997 (TREMBLREL.
01-JUL-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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STRAIN-RC-HL;
MINAMOTO N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROGLUCAGON.
                                                                                              PROGLUCAGON
                                                                                                                                                                                                                                                                                                                              Query Match
RESULT 9
ID 012955
AC 012955;
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057294
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Matches
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                                                                                                            PRELIMINARY; PRT; 178 AA.

091189; 092168; 092168; 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1999 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1999 (TREMBLREL.)
01-NOV-1999 (TREMBLREL.)
01-NOV-1996 (TREMBLREL.)
01-NOV-1996 (TREMBLREL.)
GLUCAGON 11.
EUNCHYNCHUS MYKISS (RAINBOW TROUT) (SALMO GAIRDNERI).
EUNCHYNCHA, METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII;
ELEDSTEL: EUTELEOSTEL; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95295739.

IRWIN D.M., WONG J.;

"Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";

MMOL. ENDOCRINOL. 9:267-277(1995).

EMBL: S78477; G999387;

PROSITE: PS00260; GLUCAGON; 3.
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   Gaps
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NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chery Match 49.4%; Score 114; DB 13; Length 20 Best Local Similarity 51.7%; Pred. No. 4.51e-06; Matches 15; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 120; DB 13; Length 17
Pred. No. 4.25e-07;
11; Mismatches 5; Indels
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
AC 091410
DT 01.00V-1996 (TREMBLREL. 01, CREATED)
DT 01.NOV-1996 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
DT 01.NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PROGLUCGGON.
AC GALLUS GALLUS (CHICKEN)
 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM: PF00123; hormone2; 3.
SEQUENCE 206 AA; 23875 MW; 8EC91118 CRC32;
 11; Mismatches
                                90 HADGIYISDVSIYLQDQAAKDFVSWLKSG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 HADGIYISDVSTYLQDQAAKDFVSWLKSG 118
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| hgegtftsdlskgmeeeavrlfiewlkng 29
                                                     1 hgegtftsdlskgmeeeavrlfiewlkng 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.9%;
ilarity 44.8%;
Conservative
 Conservative
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nes 13; Conserv
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 13;
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Best Loca Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLSTHOORN R.C.L., GARDE G., DAYHUFF T., ATKINS J.F., VAN DUIN J.; "Nucleotide sequence of a single-stranded RNA phage from Pseudomonas aeruginosa: kinship to coliphages and conservation of regulatory RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; LEVIVIRIDAE;
LEVIVIRUS.
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                                                                                                                                                                                                              Score 95; DB 14; Length 2127; Pred. No. 5.81e-03; 6; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                    SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: AB009663; D1024994; -.
EMBL: AB009601; D1024989; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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(023629 PRELIMINARY: PRT; 844 AA. 023629; 010-002-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 95.1 KD PROTEIN.
                                                                                                                                                                          847321FB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Match 37.2%; Score 86; DB 9; Li
Local Similarity 45.0%; Pred. No. 1.40e-01;
Les 9; Conservative 9; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIROLOGY 206;611-625(1995).
EMBL: X80191; G517241; -.
SEQUENCE 552 AA; 63300 MW; 35D63A16 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                   552 AA
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                                                                                                                                                                     242427 MW;
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                                                                                                                                                                                                                                                                                                                       9 dlskqmeeeavrlfiewlkng 29
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9 dlskqmeeeavrlfiewlkn 28
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01,
08,
                                                                                                                                                                                                              / Match 41.1%;
Local Similarity 47.6%;
Les 10; Conservative
                                                                                                                                                                                                                                                                                               37 NLNSPLIEDPVRLMLEWLKTG
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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                                                                                                                                                                     2127 AA;
                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 95133199.
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SEQUENCE FROM N.A.
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                                                              STRAIN-RC-HL;
MINAMOTO N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  structures.";
                                                                                                                                                                        SEQUENCE
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                      LT 12
Q38064
Q38064;
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PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SWALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATENSTON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., "2.2 MD of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTÄ; ENBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLLOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                  Gaps
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RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                               m
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Pred. No. 2.06e+00;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
BEVAN M., MURPHY G., DROST L., HALL C., HUDSON S., RIDLEY
BANCROFT I., MEWES H.W., MAYER K., SCHUELLER C.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBU DATA BANKS.
                                                                                                                                                                                                                                                                                               Length 844;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
EU ARABIDOPSIS SEQUENCING PROJECT;
SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, ALO21637; E1248735; -.
HYPDL, ALO21637; E1248735; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 1134 AA; 127314 MW; 1A110A00 CRC32;
SEQUENCE 1134 AA; -. SCOIE 78; DB 10; Lengt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JTN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
HYPOTHETICAL 127.3 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                        Query Match
35.1%; Score 81; DB 5; Len
Best Local Similarity 40.6%; Pred. No. 7.64e-01;
Matches 13; Conservative 10; Mismatches 6;
                                                                                                                                                                                                                                          844 AA; 95139 MW; 9A788872 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 AA
                                                                                                                                                                                                                                                                                                                                                                                        363 DPTFTSPVMYKEVEARESVPRLFLDRLVEEGF 394
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3 egtftsd-lskqmee-eav-rlfiewlknggy 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                      elegans.";
NATURE 368:32-38(1994).
BMBL; 278201; 2343300; -.
PFAM; PF00676; El déhydrog; 1.
HYPOTHETICAL PROTEIN.
SEQUENCE 844 AA; 95139 MW; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01,
07,
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Best Local Similarity 53.3%;
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
R05H5.4 PROTEIN.
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17 eavrlfiewlknggy 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MCMURRAY A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 94150718.
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049433
049433;
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Q21764
Q21764;
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MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERFY T., COOPER J., COULSON A.,
R. CRAXTON M., DEAR S., DG Z., DURBIN R., FAVELLO A., FULTON L.,
A. GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
A. JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
I.IGHTNING J., LLOYD C., MCHURRAY A., MORTINORE B., O'CALLAGHAN M.,
A. PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SUNDERS D., SHOWNKEEN R.,
A. MALDON N., SMITH A., SONNHAMMER E., STADEN R., WOHLDMAN P.,
A. THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WOHLDMAN P.,
A. ATSON A., WELNSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
I. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
B. MATURE 368:32-38(1994).
B. RABL: Z48795; E1351719; ..
B. REBL: Z48795; PROTEIN KINASE_ATP; I.
B. PROSITE; PSOOLO9; PROTEIN KINASE_ATP; I.
S. PROSITE; PSOOLO9; PROTEIN KINASE_ATP; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 77; DB 5; Length 414;
Pred. No. 2.85e+00;
9; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 35.7%;
Matches 10; Conservative
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Search completed: Mon Oct 4 15:25:30 1999 Job time: 15 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. t (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd Copyright

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 4.93 Seconds 172.374 Million cell updates/sec Mon Oct 4 15:30:19 1999; Run on:

Subular output not generated.

>монам-312-сдалм83а.РЕР (1-40) from moham312177.Рер 21-8 1 hsdgtfitsdlskqmeeeavrlfiewlknggpssgappps 40 Description: Perfect Score: Sequence:

SD

Claim Si

PAM 150 Gap 11 Scoring table:

170751 segs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries

Post-processing:

Database:

| jpart1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part119 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 30:part39 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38 39:part39

Mean 25.196; Variance 106.732; scale 0.236

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

								•							
2.62e-15	2.62e-15	2.62e-15	6.24e-15	6.24e-15	6.24e-15	6.24e-15	1.39e-12	1.47e-11	1.54e-10	8.41e-10	8.41e-10	1.59e-09	1.59e-09	3.70e-09	1.06e-08
Exendin-3, for use in	Heloderma horridum ex	Gila monster exendin-	Exendin-4, for use in	Heloderma suspectum e	Gila monster exendin-	Heloderma suspectum p	Leu(14), Phe(25)-exen	Heloderma suspectum e	Heloderma suspectum e	Exendin-4 $(1-30)$ for	Heloderma suspectum e	H. horridum exendin-3	H. horridum exendin-3	H. horridum exendin-4	H. horridum exendin-4
W61769	R80545	W47608	W61770	R80546	W47609	W70288	W61773	R80547	R80543	W61771	R80544	W39301	W39368	W39302	W39309
39	14	30	39	14	30	35	39	14	14	39	14	59	53	29	29
39	39	39	39	39	6 E	87	39	31	31	30	31	30	30	30	30
93.5	93.5	93.5	92.1	92.1	92.1	92.1	83.1	79.1	75.2	72.3	72.3	71.2	71.2	69.8	68.0
260	260	260	256	256	256	256	231	220	209	201	201	198	198	194	189
	7	М	4	Ŋ	Q	7	80	on	10	11	12	13	14	15	16
	93.5 39 W61769 Exendin-3, for use in	93.5 39 39 W61769 Exendin-3, for use in 93.5 39 14 R80545 Heloderma horridum ex	93.5 39 39 W61769 Exendin-3, for use in 93.5 39 14 R80545 Heloderma horridum ex 93.5 39 30 W47608 Gila monster exendin-	93.5 39 39 W61769 Exendin-3, for use in 93.5 39 14 R80545 Heloderma horridum ex 93.5 39 30 W47608 Gila monster exendin-92.1 39 39 W61770 Exendin-4, for use in	93.5 39.39 W61769 Exendin-3, for use in 93.5 39.14 R80545 Heloderma horridum ex 93.5 39.30 W477608 Gila monster exendin-92.1 39.34 W61770 Exendin-4, for use in 92.1 39.14 R80546 Heloderma suspectum e	93.5 39.39 W61769 Exendin-3, for use in 93.5 39.14 R80545 Heloderma horridum ex 93.5 39.30 W47608 Gila monster exendin-92.1 39.39 W61770 Exendin-4, for use in 92.1 39.30 W47609 Gila monster exendin-92.1 39.30 W47609 Gila monster exendin-	93.5 39 39 W61769 Exendin-3, for use in 93.5 39 14 R80545 Heloderma horridum ex 93.5 39 30 W47608 Gila monster exendin-92.1 39 39 W61770 Exendin-4, for use in 92.1 39 14 R80546 Heloderma suspectum e 92.1 87 35 W70288 Heloderma suspectum p	93.5 39 39 W61769 Exendin-3, for use in 93.5 39 14 R80545 Heloderma horridum ex 92.1 39 30 W47608 Gila monster exendin-92.1 39 39 W61770 Exendin-4, for use in 92.1 39 30 W47609 Gila monster exendin-92.1 39 30 W47609 Heloderma suspectum production of the second of the	93.5 39 39 W61769 Exendin-3, for use in 93.5 39 14 R80545 Heloderma horridum ex 93.5 39 30 W47608 Gila monster exendin-92.1 39 14 R80546 Heloderma suspectum e 92.1 87 35 W70288 Heloderma suspectum p 92.1 87 35 W70288 Heloderma suspectum p 83.1 39 39 W61773 Leu(14), Phe(25)-exen 79.1 31 14 R80547 Heloderma suspectum p	93.5 39 39 W61769 Exendin-3, for use in 93.5 39 14 R80545 Heloderma horridum ex 93.5 39 30 W47608 Gila monster exendin-92.1 39 39 W61770 Exendin-4, for use in 92.1 39 14 R80546 Gila monster exendin-92.1 87 35 W70288 Heloderma suspectum e 92.1 39 W6177 Leu(14), Phe(25)-exen 75.2 31 14 R80547 Heloderma suspectum e 75.2 31 14 R80543 Heloderma suspectum e 75.2	93.5 39 39 W61769 Exendin-3, for use in 93.5 39 14 R80545 Heloderma horridum ex 92.1 39 30 W477608 Gila monster exendin-92.1 39 30 W61770 Exendin-4, for use in 92.1 39 30 W47709 Gila monster exendin-92.1 87 35 W7028 Heloderma suspectum pagin 39 W61773 Leu(14), Phe(25)-exen 79.1 31 14 R80547 Heloderma suspectum pagin 14 R80547 Heloderma puspectum pagin 150	93.5 39 39 W61769 Exendin-3, for use in 83.5 39 14 R80545 Heloderma horridum ex 92.1 39 30 W47608 Gila monster exendin-92.1 39 30 W47760 Exendin-4, for use in 92.1 39 30 W47609 Gila monster exendin-92.1 39 30 W47609 Heloderma suspectum p 83.1 39 39 W61773 Leu(14), Phe(25)-exen 75.2 31 14 R80547 Heloderma suspectum e 75.2 31 14 R80543 Heloderma suspectum e 75.3 30 39 W61771 Exendin-4 (1-30) for 72.3 31 14 R80544 Heloderma suspectum e 72.3 31 14 R80545 Heloderma suspectum e 72.3 41 Heloderma suspectum e	93.5 93.5 94.7 95.5 95.6 95.6 95.7 95.1	93.5 93.9 94.80545 93.5 93.4 93.6 93.5 93.4 93.6 93.5 93.8 94.7608 93.1 93.9 94.1 93.1 94.80546 93.1 93.0 94.7700 94.1 93.0 94.7609 94.1 93.0 94.7609 94.1 93.0 94.7709 94.1 93.0 94.773 94.1 93.0 94.773 95.1 93.0 96.25 96.25 97.2 98.1 93.0 96.25 9	93.5 39 39 W61769 Exendin-3, for use in 89.5 39 14 R80545 Heloderma horridum ex 92.1 39 30 W47608 Gila monster exendin-92.1 39 30 W47700 Exendin-4, for use in 92.1 39 30 W47700 Exendin-4, for use in 92.1 39 30 W47709 Gila monster exendin-92.1 39 30 W47703 Heloderma suspectum P3.1 31 4 R80547 Heloderma suspectum exendin-4 (1-30) for 72.3 31 39 W61771 Exendin-4 (1-30) for 72.3 31 14 R80547 Heloderma suspectum exendin-3 30 29 W39301 H. horridum exendin-3 69.8 30 29 W39302 H. horridum exendin-3 69.8 horridum exendin-4 69.8 horridum

id 1.62e-0 -3 1.62e-0 -3 1.62e-0	exendin-3 1.62e-0 exendin-3 1.62e-0 exendin-4 2.00e-0 exendin-3 2.46e-0	exendin-3 2.46e-0 exendin-4 2.46e-0 exendin-3 3.04e-0 exendin-3 3.04e-0 exendin-4 3.04e-0	exendin-4 3.04e-0 exendin-3 3.04e-0 exendin-3 3.04e-0 exendin-3 3.74e-0 exendin-4 3.74e-0 exendin-4 3.74e-0	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1772 Exendin- 9369 H. horri 9370 H. horri	9420 H. horri 9305 H. horri 9331 H. horri 9371 H. horri	9378 H. horri 9312 H. horri 9383 H. horri 9406 H. horri 9332 H. horri	3317 H. horri 3330 H. horri 3389 H. horri 9404 H. horri 9403 H. horri 9327 H. horri	M39417 H. horrid M39414 H. horrid M39328 H. horrid W39408 H. horrid W39308 H. horrid W39308 H. horrid W39308 H. horrid W39308 H. horrid W39308 H. horrid
7.3 28 3 7.3 30 2 7.3 30 2	77.3 77.3 80.0 80.0 80.0 80.0 80.0 80.0	66.5 30 20 20 20 20 20 20 20 20 20 20 20 20 20	66.2 66.2 86.2 86.2 86.2 86.2 86.2 86.2	665.8 66
7 18 8 18 9 18	0 1 1 8 1 1 1 1 8 1	98465	0 1 1 8 1 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	37 338 338 339 440 441 444 443 183 183 183

ALIGNMENTS

Deeley NRA, Bhayast S, Prickett KS;

Beeley NRA, Bhayast S, Prickett KS;

Reducing food intake by administering exendins or their

Reducing food intake by administering exendins or their

analogues - for treatment of e.g. obesity, type II diabetes,

eating disorders and insulin resistance

analogues 0, 24; Page 8, 214pp; English.

The invention relates to a new method for treating disorders that

are alleviated by reducing food intake, in particular obesity, type

II diabetes, eating disorders, insulin resistance syndrom, elevated

plasma glucose levels, or the risk of cardiac disease. The method

comprises administering an exendin or an exendin agonist. The treatment

reduces appetite and lowers plasma lipid levels. If inhibits food

consumption as effectively as amylin or cholecystokinin but has a much

longer-lasting action (still effective after 6 hours in a mouse model).

The present sequence is that of exendin-3 which is one of the preferred

compounds for use in the method. Exendin-3, for use in treating disorders related to food intake. Exendin; obesity; type II diabetes; eating disorders; cardiac disease; insulin resistance syndrome; elevated plasma glucose level; agonist. T W61769 standard; peptide; 39 AA. 29-MAR-1999 (first entry) (AMYL-) AMYLIN PHARM INC 14-NOV-1997; US-066029. 07-JAN-1997; US-034905. 08-AUG-1997; US-055404. 14-NOV-1997; US-065442 07-JAN-1998; U00449 Heloderma horridum WO9830231-A1 RESULT

1; Score 260; DB 39; Length 39; Pred. No. 2.62e-15; 0; Mismatches 0; Indels Query Match
Best Local Similarity 97.5%;
Matches 39; Conservative

Gaps

hsdgtf-tsdlskgmeeeavrlfiewlknggpssgappps 39

셤

1 hsdgtfitsdlskqmeeeavrlfiewlknggpssgappps 40

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Eng J;
WPI; 95-262627/34.
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                    W61770
                                                                                                                                       Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                     Stimulating/inhibiting insulin release with exendin polypeptide(s) - for treating diabetes mellitus and preventing hyperglycaemia.

Claim 5. Columns 13-14; 17pp; English.

R80545 is Heloderma horridum exendin-3. It is an insulinotropic peptide, and can therefore be used in the treatment of diabetes mellitus (types I or II), and for the prevention of hyperglycaemia. It normalises hyperglycaemia through glucose-dependent sequence 39 AA;
                                                                     27-FEB-1996 (first entry)
Heloderma horridum exendin-3.
Exendin-3; diabetes mellitus; hyperglycaemia; insulinotropic peptide.
US5424286-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-AUG-1996; US-654954.

(AMYL-) AMYLIN PHARM INC.
Beelbey NRA, Gedulin B, Prickett KS, Young AA;
WPI: 98-145551/13.

Regulating gastrointestinal motility using exendins or their agonists - for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations impaired glucose tolerance etc., rightsh.

W47549 describes a generic exendin agonist, provided that it does have the formula of either exendin-3 (W47608) or exendin-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exendin agonists, which reduce gastric motility and delay gastric emptying, can be used to treat spasm (where associated with acute diverticulities or disorders of the biliary tract or sphincter of oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. They can also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic resonance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exendin agonist; gastric motility; gastric emptying; treatment; spasm, postprandial dumping syndrome; postprandial hyperglycaemia; type I diabetes; impaired glucose tollerance; toxin ingestion; obesity; Gila monster venom; exendin-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 260; DB 14; Le
Pred. No. 2.62e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 hsdgtf-tsdlskqmeeeavrlfiewlknggpssgappps 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W47608 standard; peptide; 39 AA
  T 2
R80545 standard; peptide; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.5%;
97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUL-1998 (first entry) Gila monster exendin-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39; Conservative
                                                                                                                                                                                                                         24-MAY-1993; 066480.
24-MAY-1993; US-066480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-FEB-1998.
08-AUG-1997; U14199
08-AUG-1996; US-6949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heloderma horridum.
                                                                                                                                                                                                                                                                                                                     95-262627/34
                                                                                                                                                                                                                                                                     (ENGJ/) ENG J.
Eng J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified_site
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                                                                                                                                                                                                  13-JUN-1995
                                                     R80545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (W47609)
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RESULT
ID R8
AC R8
DT 27
DE H6
CS RW EX
CS RW EX
CS RW DD US
PD US
PR 24
PR 24
PR 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analogues - for treatment of e.g. obesity, type II diabetes, eating disorders and insulin resistance cating disorders and insulin resistance claims 17, 25, page 8: 214pp; English.

The invention relates to a new method for treating disorders that are alleviated by reducing food intake, in particular obesity, type II diabetes, eating disorders, insulin resistance syndrome, elevated plasma glucose levels, or the risk of cardiac disease. The method comprises administering an exendin or an exendin agonist. The treatment comprises appetite and lowers plasma lipid levels. If inhibits food consumption as effectively as amylin or cholecystokinin but has a much longer-lasting action (still effective after 6 hours in a mouse model). The present sequence is that of exendin-4 which is one of the preferred sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-1999 (first entry)
Exendin-4, for use in treating disorders related to food intake.
Exendin: obesity: type II dlabetes: eating disorders; cardiac disease; insulin resistance syndrome; elevated plasma glucose level; agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-1996 (first entry)
Heloderma suspectum exendin-4.
Exendin-4; diabetes mellitus; hyperglycaemia; insulinotropic peptide.
Heloderma suspectum.
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
             Exendins, components of Gila monster venom, have some sequence similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and sequence 39 AA;
                                                                                                                                                                                                                                 ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                         Score 260; DB 30; Length 39;
Pred. No. 2.62e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 39; Length 39;
                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reducing food intake by administering exendins or their
                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                              39
                                                                                                                                                                                                                                                                                                      Score 256; DB 39; 1
Pred. No. 6.24e-15;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hgegtf-tsdlskqmeeeavrlfiewlknggpssgappps 39
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                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beeley NRA, Bhavsar S, Prickett KS;
WPI; 98-398796/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 5
R80546 standard; peptide; 39 AA.
R80546;
                                                                                                                                                                         93.5%;
Local Similarity 97.5%;
les 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 92.1%;
Best Local Similarity 92.5%;
Matches 37; Conservative
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07-JAN-1998.

07-JAN-1997. US-066029.

07-JAN-1997; US-034905.

08-AUG-1997; US-055404.

14-NOV-1997; US-065442.

(AMIL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-1993; 066480.
24-MAY-1993; US-066480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heloderma suspectum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUN-1995
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3

Matches

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PSDB; V33163.

N-PSDB; V33163.

N-PSDB; V33163.

N-PSDB; V33163.

N-PSDB; V33163.

N-PSDB; V33163.

New nucleic acid encoding proexendin - used to diagnose and treat, e.g. endocrine tumours, also to treat poisoning by reptile venome term as uspectum proexendin peptide is encoded by its cDNA thich was isolated from a H. suspectum salivary gland cDNA library. The proexendin protein comprises of a novel exendin N-terminal which was isolated from a H. suspectum salivary gland cDNA library. The proexendin protein comprises of a novel exendin N-terminal peptide (ENTP) linked to the N-terminus of the exendin A peptide

The proexendin peptids to ridentify related sequences (e.g. the cannot be used to clone or identify related sequences (e.g. the cannot be used to clone or identify related sequences (e.g. the cannot great and species of gene regulatory defects associated with metabolic disease) and species homologues (e.g. for developing animal models for drug screening).

The proexendin peptide can be used to raise antibodies. Anti-proexendin antibodies are claimed to be useful for diseases and organ failure), for identifying other regulators of cell metabolism, in drug screens and for treating metabolic diseases (e.g. diabetes) and for neutralising, or detecting, reptillan venom peptides.
                                                                  Heloderma suspectum proexendin peptide.

Heloderma suspectum proexendin; exendin N-terminal peptide; ENTP;
exendin 4 peptide; exendin 3 gene; Heloderma horridum; metabolic disease;
drug screening; endocrine tumour; organ failure; cell metabolism;
Heloderma suspectum.
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Dipeptidyl peptidase cleavage site"
                                                                                                                                                                                                                                                        1..23
/note= "Signal peptide"
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                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          48..87
/note= "Exendin 4"
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W61773 standard; peptide; 39 AA.
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                                                                                                                                                                                                                                                                                                                             /note= "ENTP"
W70288 standard; Protein; 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ONEO-) 1149336 ONTARIO INC.
Drucker DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 92.1%;
Best Local Similarity 92.5%;
Matches 37; Conservative
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       46..47
/note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1998.
04-FEB-1998; CA0071.
07-FEB-1997; GB-002582.
05-FEB-1997; US-037412.
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                                                  06-NOV-1998
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                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W61773;
                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                          Peptide
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     ij
                                                                                                                                                                                                                                                                                                       Ĥ,
                  for treating diabetes mellitus and preventing hyperglycaemia. Claim 6; Columns 13-14; 17pp; English.
R80546 is Heloderma suspectum exendin-4. It is an insulinotropic peptide, and can therefore be used in the treatment of diabetes mellitus (types I or II), and for the prevention of hyperglycaemia. It normalises hyperglycaemia through glucose-dependent and insulin-(in)dependent mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-AUG-1996; US-694954.

(AMYL-) AMYLIN PHARM INC.
Beeley NRA, Gedulin B, Prickett KS, Young AA;
Beeley NRA, Gedulin B, Prickett KS, Young AA;
WWPI; 98-145351/13.

Regulating gastrointestinal motility using exendins or their agonists - for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations injained glucose tolerance etc., also in diagnostic investigations (india) 20 and 21; Fig 1: 70pp; English
W47549 describes a generic exendin agonist, provided that it does have the formula of either exendin-3 (W47608) or exendin-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exendin agonists, which reduce gastric motility and delay gastric emptying, can be used to treat spasm (where associated with acute diverticulitis or disorders of the buliary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. They can also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic resonance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exendin agonist; gastric motility; gastric emptying; treatment; spasm, postprandial dumping syndrome; postprandial hyperglycaemia; type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity; Gila monster venom; exendin-4.
Stimulating/inhibiting insulin release with exendin polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exendins, components of Gila monster venom, have some sequence similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.

Sequence 39 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
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                                                                                                                                                                                                                                                   Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                   Score 256; DB 14; Length 39 Pred. No. 6.24e-15; 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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ID W47609 standard; peptide; 39
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Similarity 92.5%;
37; Conservative
                                                                                                                                                                                                                                                   Similarity 92.5%; 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-1998 (first entry) Gila monster exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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08-AUG-1997; U14199.
                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heloderma suspectum
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                                                                                                                                                                                                                                                     Query Match
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Leu(L4), Phe(25)-exendin-4 amide, for reducing food intake.
Exendin, obesity; type II diabetes; eating disorders; cardiac disease;
insulin resistance syndrome; elevated plasma glucose level; agonist.
                                                                                                                                                                                          Gaps
                                                                                                                                                                                    Ξ,
                                                                Length 87;
Score 256; DB 35; Length o'.
Pred. No. 6.24e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "the C-terminal is in amide form"
                                                                                                                                                                                                                                                                                                                                                                               48 hgegtf-tsdlskqmeeeavrlfiewlknggpssgappps 86
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US-066029.
US-034905.
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14-NOV-1997; 07-JAN-1997; 1
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Matches

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NEELEY NEW, Bhavers JAC.

Beeley NEW, Bhavers S, Prickett KS;

WEI; 98-398796/34.

Reducing food intake by administering exendins or their
Reducing food intake by administering exendins or their
analogues - for treatment of e.g. obesity, type II diabetes,
eating disorders and insulin resistance
The invention relates to a new method for treating disorders that
The invention relates to a new method for treating disorders that
The invention relates to a new method for treating disorders that
The invention relates to a new method for treating disorders,
If diabetes, eating disorders, insulin resistance syndrome, elevated
Indiabetes, eating disorders, insulin resistance syndrome, elevated
Comprises administering an exendin or an exendin agonist. The treatment
reduces appetite and lowers plasma lipid levels. It inhibits food
consumption as effectively as amylin or cholecystokinin but has a much
longer-lasting action (still effective after 6 hours in a mouse model).
The present sequence is that of an exendin-4 variant which is one of
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Stimulating/inhibiting insulin release with exendin polypeptide(s) Stimulating/inhibiting insulin release with exendin polypeptide(s) for treating diabetes mellitus and preventing hyperglycaemia.

Claim 7: Columns 13-14: 17pp: English.

R80547 is the Heloderma suspectum exendin-4 residues 9-39. It is an insulinotropic peptide activity inhibitor.

Sequence 31 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-FEB-1996 (first entry)
Beloderma suspectum exendin-4 residues 9-39 (Extendin-4(9-39)).
Exendin-4; residues 9-39; Exendin-4(9-39);
Insulinotropic peptides; inhibitor.
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H
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Heloderma suspectum exendin-4 residues 1-31 (Exendin-4(1-31)).
Exendin-4: residues 1-31; Exendin-4(1-31); diabetes mellitus; hyperglycaemia; insulinotropic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                     Score 231; DB 39; Length 39;
Pred. No. 1.39e-12;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 220; DB 14; Length 31;
Pred. No. 1.47e-11;
0; Mismatches 0; Indels
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R80547 standard; peptide; 31 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                   Match 83.18;
Local Similarity 87.58;
Nes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.1%;
Local Similarity 100.0%;
Nes 31; Conservative
                                      (AMYL-) AMYLIN PHARM INC
08-AUG-1997; US-055404.
14-NOV-1997; US-065442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-1993; 066480.
24-MAY-1993; US-066480.
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24-MAY-1993; 066480.
24-MAY-1993; US-066480.
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                                                                                                                                                                                                                                                                                                                                                            Sequence
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Best Local 9
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                           Stimulating/inhibiting insulin release with exendin polypeptide(s) - for treating diabetes mellitus and preventing hyperglycaemia. Claim 1; Columns 13-14; 17pp; English. R80543 is the Heloderma suspectum exendin-4 residues 1-31. It is an insulinotropic peptide, and can therefore be used in the treatment of diabetes mellitus (types I or II), and for the prevention of hyperglycaemia. It normalises hyperglycaemia through glucose-dependent and insulin-(in)dependent mechanisms.
                                                                                                                                                                                                                                                                     29-MAR-1999 (first entry)
Exendin-4 (1-30) for use in treating disorders related to food intake.
Exendin; obesity, type II diabetes; eating disorders; cardiac disease; insulin resistance syndrome; elevated plasma glucose level; agonist.
                                                                                                                                                                  Gaps
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H
                                                                                                                                           Length 31;
                                                                                                                              Score 201; DB 39; Length 30;
Pred. No. 8.41e-10;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R80544;
27-FEB-1996 (first entry)
Heloderma suspectum exendin-4 residues 1-31-Tyr31.
                                                                                                                                                                                 1 hgegtf-tsdlskgmeeeavrlfiewlknggp 31
                                                                                                                                                                                            1 hgegtf-tsdlskqmeeeavrlfiewlkngg 30
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                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                       JI 11
W61771 standard; peptide; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R80544 standard; peptide; 31 AA.
                                                                                                                                       h 75.2%;
Similarity 90.6%;
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.3%;
Best Local Similarity 90.3%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              14-NOV-1997; US-066029.
07-JAN-1997; US-034905.
                                                                                                                                      Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                  Heloderma suspectum,
                                                                                                                                                                                                                                                                                                                                                                        16-JUL-1998.
07-JAN-1998; U00449.
                    WPI; 95-262627/34
                                                                                                                   Sequence 31 AA;
(ENGJ/) ENG J.
Eng J;
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WO9746584-A1.
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                                                                                     RESULT STATE OF THE STATE OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This peptide is a fragment of exendin-3 isolated from Heloderma horridum. This peptide and its salts, esters and derivatives can be horridum. This peptide and its salts, esters and derivatives can be suced to treat diabetes mellitus. They stimmlate biosynthesis and secretion of insulin, but have the opposite effect on glucagon, and independent of this activity can increase peripheral glucose utilisation. Exendin-3 and exendin-4 are only active when blood sugar levels are high, so they will not induce hypolycaemia. Compared with glucagon-like peptide 1 (GLP1) and the known exendins, they are more active (effective longer lasting effect. Truncated forms of this peptide can be made more sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ĥ
                                                                                                                                                                                                                                WELL 95-262627/34.
Stimulating/inhibiting insulin release with exendin polypeptide(s) -
Stimulating/inhibiting insulin release with exendin polypeptide(s) -
Lor treating diabetes mellipts and preventing hyperglycaemia.
Claim 2: Columns 13-14: 17pp; English.
R80544 is the Heloderma suspectum exendin-4 residues 1-31, where
the native Pro31 has been replaced with a Tyr residue. It is an
insulinotropic peptide, and can therefore be used in the treatment of
diabetes mellitus (types I or II), and for the prevention of
hyperglycaemia. It normalises hyperglycaemia through glucose-dependent
Sequence 31 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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increase secretion and biosynthesis of insulin, but reduce those of
glucagon, and do not induce hypoglycaemia
Claim 1; Page 3; 150pp; English.
Exendin-4; residues 1-31; Y-31-Exendin-4(1-31); diabetes mellitus;
hyperglycaemia; Tyr31; insulinotropic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W39301;
905-JUN-1998 (first entry)
H. horridum exendin-3 peptide.
Exendin-3; exendin 4; diabetes; insulin; secretion; biosynthesis; glucagon reduction; hypoglycaemia; glucose; treatment.
Heloderma horridum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _note= "This residue can be any amino acid except
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 31;
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Pred. No. 8.41e-10;
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Goeke B, Goeke R, Hoffmann E;
WPI; 98-042119/04.
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Local Similarity 90.3%;
les 28; Conservative
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Best Local Similarity 96.7%;
Matches 29; Conservative
                                                                                                   13-JUN-1995.
24-MAY-1993; 066480.
24-MAY-1993; US-066480.
(ENGJ/) ENG J.
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05-JUN-1996; DE-022502.
                                                       Heloderma suspectum
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05-JUN-1997; E02930.
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Gaps

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1 hsdgtf-tsdlskqmeeeavrlfiewlkng 29

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glucagon, and do not induce hypoglycaemia collaim 2; page 27; 150pp; Bnglish.
Peptides w3930-W39420 are fragments of exendin-3 and exendin-4 isolated from Heloderma horidum which are used in a novel method for the treatment of diabetes mellitus. These peptides can stimulate biosynthesis and secretion of insulin, but have the opposite effect on glucagon, and independent of this activity can increase peripheral glucose utilisation. Exendin-3 and exendin-4 are only active when blood sugar levels are high, so they will not induce hypoglycaemia. Compared with glucagon-like peptide 1 (GIPI) and the known exendins, they are more active (effective at lower doses), more stable to degradation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metabolism and have a longer lasting effect. Truncated forms of this peptide can be made more economically than full length versions. Sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Truncated versions of exendin peptide(s) for treating diabetes - increase secretion and biosynthesis of insulin, but reduce those of
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GOEKE B, GOEKE R, HOffmann B;
WPI; 98-042119/04.
Truncated versions of exendin peptide(s) for treating diabetes increase secretion and blosynthesis of insulin, but reduce those of
                                                                      H. horridum exendin-3 peptide derivative #11.
Exendin-3; exendin 4; diabetes; insulin; secretion; biosynthesis;
glucagon reduction; hypoglycaemia; glucose; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H. horridum exendin-4 peptide.
Exendin-3: exendin 4; diabetes; insulin; secretion; biosynthesis;
glucagon reduction; hypoglycaemia; glucose; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note- "This residue can be any amino acid except Gly"
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Claim 1; Page 4; 150pp; English.
This peptide is a fragment of exendin-4 isolated from Heloderma
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05-UUN-1997; E02930.
13-SEP-1996; DE-037230.
05-UUN-1996; DE-022502.
(BOEF ) BOEHRINGER MANNHEIM GMBH.
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W39302 standard; peptide; 30 AA.
W39302;
W39368 standard; peptide; 30 AA.
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Best Local Similarity 96.7%;
Matches 29; Conservative
                       W39368;
05-JUN-1998 (first entry)
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05-JUN-1997; E02930.
13-SEP-1996; DE-037230.
05-JUN-1996; DE-022502.
                                                                                                                                                 Heloderma horridum.
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horridum. This peptide and its salts, esters and derivatives can be used to treat diabetes mallitus. They stimulate blosynthesis and insed to treat diabetes mallitus. They stimulate blosynthesis and independent of this activity can increase peripheral glucose utilisation. Exendin-3 and exendin-4 are only active when blood sugar levels are high, so they will not induce hyposylvaemia. Compared with glucagon-like peptide 1 (Girl) and the known exendins, they are more active (effective at lower doses), more stable to degradation and metabolism and have a longer lasting effect. Truncated forms of this peptide can be made more sconomically than full length versions.
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Gaps Ĥ Score 194; DB 29; Length 30; Pred. No. 3.70e-09; 2; Mismatches 0; Indels Query Match
Best Local Similarity 90.0%;
Matches 27; Conservative

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Search completed: Mon Oct 4 15:30:39 1999 Job time: 20 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Oct 4 15:29:52 1999; MasPar time 4.88 Seconds 328.404 Million cell updates/sec Run on:

mabular output not generated. Lie: Description: Perfect Score: Sequence:

>MOHAM-312-CLAIM83A.PEP (1-40) from moham312177.pep 278 1 hsdytfitsdlskqmeeeavrlfiewlknggpssgappps 40

PAM 150 Gap 11 Scoring table:

122810 seqs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 35.024; Variance 64.745; scale 0.541

SUMMARIES

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Score	1	Query Match	Query Match Length	DB	ID	Description	Pred. No.
260		93.5	39	7	HWGH3Z	exendin-3 - Mexican b	7.55e-34
256		92.1	39	Н	HWGH4G	ı	4.98e-33
118		42.4	101	Н	GCFGB	pre	1.45e-06
117		42.1	31	~	S44472		2.15e-06
116		41.7	63	٦	GCIDC	glucadon precursor -	3.18e-06
113		40.6	30	7	S44473		1.02e-05
112		40.3	31	7	S44471	lucadon G1 -	1.49e-05
111		39.9	99	7	151093	glucadon - chinook sa	2.19e-05
111		39.9	178	7	151058	н	2.19e-05
111		39.9	178	~	151057	lucagon	2.19e-05
110		39.6	30	~	C61125	Ξ	3.21e-05
110		39.6	30	~1	B61125	glucagon-like peptide	3.21e-05
110		39.6	72	Н	GCGXA	glucadon precursor -	3.21e-05
109		39.5	122	~1	GCAF2		4.70e-05
108		38.8	9	Н	GCONC	Д	6.87e-05
106		38.1	29	Н	GCDF	glucadon - smaller sp	1.46e-04
104		37.4	124	Н	GCAF	lucagon 1 precurso	3.09e-04
104		37.4		Н	GCPG	ď	3.09e-04
104		37.4		Н	GCRT		3.09e-04
104		37.4	180	Н	GCRIDU	glucagon precursor -	3.09e-04
104		37.4	180	Н	GCBO	glucagon precursor -	3.09e-04
104		37.4	180	Н	GCHY	glucagon precursor -	3.09e-04
104		37.4	180	Н	GCGP	glucagon precursor -	3.09e-04

37.4 180 1 GCHU glucagon precursor - 3.09e-04 37.1 151 1 GCCH glucagon precursor - 3.09e-04 37.1 206 2 151301 proglucagon - Chicken 4.47e-04 36.0 29 2 S07211 glucagon - Chicken 1.35e-03 34.2 29 1 GCCB glucagon - Chicken 1.35e-03 34.2 29 2 A61135 glucagon - Duropean f 8.25e-03 34.2 29 2 A61135 glucagon - Digeye tun 8.25e-03 34.2 29 2 A61135 glucagon - Digeye tun 8.25e-03 32.4 29 2 A61135 glucagon - Digeye tun 8.25e-03 32.4 29 2 A61135 glucagon - Common squ 4.81e-02 32.4 29 1 GCDEN glucagon - Common squ 4.81e-02 32.4 29 2 GS958 glucagon - Common squ 4.81e-02 32.4 29 2 GS9048 glucagon - Arabian ca 4.81e-02 32.4 69 1 GCD69 glucagon - Arabian ca 4.81e-02 31.7 2127 1 ZLYNRS genome polyproctein - 9.59e-02 31.7 2127 1 ZLYNRS genome polyproctein - 9.59e-02 30.9 29 2 A91740 glucagon - Lurkey (te 1.90e-01 30.9 52 1 A61583 glucagon - North Amer 1.90e-01 30.9 52 1 A61583 glucagon - Ostrich 2.66e-01	HWGH3Z #type c exendin-3 - Mexica #formal_name Helod lizard 31-Mar-1993 #seque 21-Nov-1997 A23674 A23674 Bng, J.; Andrews, J. Biol. Chem. (19 Purification and s secretagogue iso rences WIID:91056067 A23674	1-39 #label ENG Ins are venom components that are the vascactive intestinal peptide and/on ar cells and to activate adenylate retion of amylase. #superfamily glucagon amidated carboxyl end; duplication; #modified_site amidated carbox experimental #length 39 #molecular-weight 4204 93.5%; Score 260; DB 1; ilarity 97.5%; Pred. No. 7.55e-34; Conservative 0; Mismatches 0	### Transport
224 225 24 255 27 27 27 27 27 27 27 27 27 27 27 27 27	RESULT 1 ENTRY ONGANISM DATE ACCESSIONS REFERENCE #journal #title #cross referen #accession #accession #accession #accession ##molecule_ ##molecule_ ##molecule_ ##molecule_ ##molecule_ ##molecule_ ##molecule_ ##molecule_	##resid MMENT EX ASSIFICATIO YWORDS ATURE 39 MMARY Query Match Best Local	Db 1 HSDGTF QY 1 hsdgtf QY 1 hsdgtf RESULT 2 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors

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hsdgtfitsdlskqmeeeavrlfiewlknggp 32
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Best Local Similarity
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ORGANISM
DATE
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30-63
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                                                                                                                               sidues 1-39 ##label ENG
Exendin-4 does not stimulate amylase secretion by pancreatic acinar
J. Biol. Chem. (1992) 267:7402-7405
Isolation and characterization of exendin-4, an exendin-3
analogue, from Heloderma suspectum venom. Further evidence
for an exendin receptor on dispersed acini from guinea pig
                                                                                                                                                                                                                                                                                                                                         Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucagon; glucagon-36 (oxyntomodulin); glucagon-like peptide
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#rabel GLI\
#label GLI\
#label GLI\
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*product glucagon-like peptide 1 #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Pollock, H.G.; Hamilton, J.W.; Rouse, J.B.; Ebner, K.E.;
Rawitch, A.B.

#journal J. Biol. Chem. (1988) 263:9746-9751

#title Jobation of peptide hormones from the pancreas of the bullfrog (Rana catesbelana). Amino acid sequences of pancreatic polypeptide, oxyntomodulin, and two glucagon-like peptides.

*cross-references MUID:88257102

*accession. B28091
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bullfrog
#text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type protein
##residues 69-101 ##label PO3
fPICATION #superfamily glucagon
abs carbohydrate metabolism; duplication; hormone; pancreas
                                                                                                                                                                                                                               #modified_site amidated carboxyl end (Ser) #status
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                                                                                                                                                                                                                                                *Product glucagon-36 (oxyntomodulin) *status
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Pred. No. 1.45e-06;
7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                      Length 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; glucagon-like peptide 2
#formal_name Rana catesbeiana #common_name
31-Mar-1993 #sequence_revision 31-Mar-1993
                                                                                                                                                                                #superfamily glucagon
amidated carboxyl end; duplication; venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCFGB #type fragments
glucagon precursor - bullfrog (fragments)
                                                                                                                                                                                                                                                                                                                                                                                  1 HGEGIF-TSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS 39
                                                                                                                                                                                                                                                                                                 Score 256; DB 1; Pred. No. 4.98e-33;
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B28091; C28091; D28091
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##residues 37-68 ##label POL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type protein
##residues 1-36 ##label PO2
                                                                                  #cross-references MUID:92218391
#accession A42486
                                                                                                                                                                                                                                                                                                 92.1%;
larity 92.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.1%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oxyntomodulin
                                                                                                            ##molecule_type protein
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nes 37; Conser
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Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M. Blochem. J. (1994) 300:339-345
Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (Polyodon spathula).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glucagon precirsor - channel catfish (fragments)
#formal_name Ictalurus punctatus #common_name channel catfish
31.Mar-1993 #sequence_revision 31-Mar-1993 #text_change
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#product glucagon-like peptide 1 #status experimental
#label GL1
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##residues 30-63 ##label AND2
FPICATION #superfamily glucagon
UDS carbohydrate metabolism; duplication; hormone; pancreas
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#journal J. Biol. Chem. (1985) 260:3910-3914
#title Isolation and structures of glucagon and glucagon-like
#cross-references MUID:85157536
                                                                                                                                                                                                                                                                                                                                                                                                             #product glucagon G2 #status predicted #label
#length 31 #molecular-weight 3682 #checksum 7826
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Pred. No. 3.18e-06;
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##residues 1-29 ##label AND1
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50.0%;
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RESULT

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#authors Irwin, D.M.; Wong, J.
#journal Mol. Endocrinol. (1995) 9:267-277
#title Trout and chicken proglucagon: alternative splicing generates
#cross-references MUID:95295739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucagon I precursor - rainbow trout
#formal_name Oncorhynchus myklss #common_name rainbow trout
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
21-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-178 ##label IRW
##cross-references EMBL:U19917; NID:9736364; PID:9736365; GB:S78475;
NID:9999384; PID:9999385
                                                                                                                                                                                                                                                                                                     Gaps
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#journal Mol. Endocrinol. (1995) 9:267-277
#title Trout and chicken proglucagon: alternative splicing mRNA transcripts encoding glucagon-like peptide 2.
#cross-references MUID:95295739
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##molecule_type mRNA
###____solute_type mRNA
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A55895
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5R-172 4.*.
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##molecule_type mRNA
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##molecule_type DNA
##residues 'M',114-144 ##label IR4
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preliminary; translated from GB/EMBL/DDBJ
##noleoule_type DNA
##residues
113-123 ##label IRS
##cross-references EMBL:U19918; NID:g736373; PID:g736376
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Pred. No. 2.19e-05;
"".marrhes 5; Indels
                                                                                                                                                                        NID:9736366; PID:9736367
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                                                                                                                                                                                                          duplication
#length 66 #checksum 1440
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Best Local Similarity 46.7%;
Matches 14; Conservative
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Best Local Similarity 46.7%;
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                                                                                                                                    Nguyen, T.M.; Momusen, T.P.; Mims, S.M.; Conlon, J.M.
Blochem. J. (1994) 300:339-345
Characterization of insulins and proglucagon-derived peptides
from a phylogenetically ancient fish, the paddlefish
(Polyodon spathula).
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Blochem. J. (1994) 300:339-345
Characterization of insulins and proglucagon-derived peptides
from a phylogenetically ancient fish, the paddlefish
(Polyodon spathula).
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glucagon G1 - North American paddlefish (Polyodon spathula)
formal_mame Polyodon spathula
18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change
20-Mar-1998
   S44473 #type complete
glucagon-like peptide - North American paddlefish (Polyodon
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18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change
20-Mar-1998
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##experimental_source pancreas
FICATION #superfamily glucagon
DS carbohydrate metabolism; duplication; hormone; pancreas
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Pred. No. 1.49e-05;
"":matches 7; Indels
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Pred. No. 1.02e-05;
6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                   #molecular-weight 3359
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#superfamily glucagon
duplication; hormone; pancreas
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llarity 56.7%;
Conservative
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Best Local Similarity 56.7%;
Matches 17; Conservative
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#length 30
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Query Match 39.6%;
Best Local Similarity 43.3%;
Matches 13; Conservative
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                                                                                                                                                                                    151057 *type complete
glucagon II precursor - rainbow trout
#formal_name Oncorhyntus myxiss #common_name rainbow trout
13.5ep-1996 #sequence_revision 13-Sep-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Conlon, J.M.; Andrews, P.C.; Thim, L.; Moon, T.W.
#journal Gen. Comp. Endocrinol. (1991) 82:23-32
#title The primary structure of glucagon-like peptide but not insulin has been conserved between the American eel, Anguilla rostrata and the European eel, Anguilla anguilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucagon-like peptide - European eel
#formal_name Anguilla anguilla #common_name European eel
10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *product glucagon-like peptide *status experimental *label GLP\
*modified_site amidated carboxyl end (Arg) *status
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#superfamily glucagon
duplication
#length 178 #molecular-weight 19998 #checksum 4464
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Pred. No. 2.19e-05;
10; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                  ##residues 1-178 ##label IRW
##cross references EMBL:U19914; NID:g736362; PID:g736363
cession I51039
                                                                                                                                                                                                                                                                                                                                                                                      #superfamily glucagon
amidated carboxyl end; duplication
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| hsdgtfitsdlskqmeeeavrlfiewlkng 30
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Local Similarity 46.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Conlon, J.M.; Andrews, P.C.; Thim, L.; Moon, T.W.
#journal Gen. Comp. Endocrinol. (1991) 82:23-32
#title The primary structure of glucagon-like peptide but not
   insulin has been conserved between the American eel,
Anguilla rostrata and the European eel, Anguilla anguilla.
#cross-references MUID:91340068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Pollock, H.G.; Kimmel, J.R.; Ebner, K.E.; Hamilton, J.W.;
Rouse, J.B.; Lance, V.; Rawitch, A.B.
#journal Gen. Comp. Endocrinol. (1988) 69:133-140
#title Isolation of alligator gar (Lepisosteus spatula) glucagon, Oxyntomodulin, and glucagon-like peptide: amino acid sequences of oxyntomodulin and glucagon-like peptide.
#Cross_references MUID:88196798
                                                                                                                                                                                                                                                                 glucagon-like peptide - American eel #formal_name Anguilla rostrata #common_name American eel 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *product glucagon-like peptide *status experimental *label GLP.
*modified site amidated carboxyl end (Arg) *status predicted
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##molecule_type protein
##residues 39-72 ##label PO2
##residues 39-72 ##label PO2
##residues 37-38 represent a pair of basic amino acids forming a cleavage site.
LASSIFICATION #superfamily glucagon carbohydrate metabolism; duplication; hormone; pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #formal_name Lepisosteus spatula #common_name alligator
31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
20-Mar-1998
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                    Length 30;
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Pred. No. 3.21e-05;
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glucagon precursor - alligator gar (fragment)
Score 110; DB 2; Les
Pred. No. 3.21e-05;
'''-matches 6;
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amidated carboxyl end; duplication
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Best Local Similarity 43.3%;
Matches 13; Conservative
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#journal Regul. Pept. (1986) 14:57-67
#title Regul and structure of coho salmon (Oncorhynchus kisutch)
#cross-references MulD:86234328
#accession JP0103
##molecule_type protein
##residues 1-29;30-60 ##label PLI
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glucagon; glucagon-11ke peptide 1
formal_mame Oncorhynchus Kisutch #common_name coho salmon
30-sep-1988 #sequence_revision 30-Sep-1988 #text_change
20-Mar-1998
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*product proglucagon 2 *status predicted *label PGC2\
*product glucagon *status predicted *label GCN\
*product glucagon-like peptide 1 *status predicted
*label GLI
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##molecule_type mRNA
##residues 1-122 ##label LUN
##cross-references GB:J00933; NID:g213352; PID:g213353
CLASSIFICATION #superfamily glucagon
KEYWORDS carbohydrate metabolism; duplication; hormone; pancreas
Gaps
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31-Mar-1993 *sequence_revision 31-Mar-1993 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Lund, P.K.; Goodman, R.H.; Montminy, M.R.; Dee, P.C.;
Habener, J.F.
#journal J. Biol. Chem. (1983) 258:3280-3284
#title Anglerfish islet pre-proglucagon II. Nucleotide and corresponding amino acid sequence of the cDNA.
#accession A05150
                                                                                                                                                                                                                                                                                                       #length 122 #molecular-weight 14171 #checksum 7194
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                                                                                                                          39.6%; Score 110; DB 1; Length 72; larity 46.7%; Pred. No. 3.21e-05; Conservative 9; Mismatches 6; Indels
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protein - protein database search, using Smith-Waterman algorithm Mon Oct 4 15:28:55 1999; MasPar time 3.27 Seconds 346.176 Million cell updates/sec Run on:

mabular output not generated.

MPsrch_pp

>MOHAM-312-CLAIM83A.PEP (1-40) from moham312177.pep 278 1 hsdgtfitsdlskqmeeeavrlfiewlknggpssgappps 40 cle: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 35.894; Variance 59.375; scale 0.605 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	-	Score	Query Match	Query Match Length	DB	Ð	Description	u C	Pred. No.	
;	Н	260	93.5	39	Н	EXE3 HELHO	EXENDIN-3.	• • • • • • • • • • • • • • • • • • •	7.016-38	
	7	256	92.1	87	Н	EXE4 HELSU	EXENDIN-4	PRECURSOR	5 736-37	
,	m	118	42.4	103	Н	GLUC_RANCA	GLUCAGON	PRECURSOR (FR	•	
	4	117	42.1	71	٦	GLUC_ICTPU	GLUCAGON	PRECURSOR (FR	H	
	Ŋ	110	39.6	30	П	GLUM ANGAN	GLUCAGON-1	LIKE PEPTII	m	
	9	110	39.6	78	Н	GLUC_LEPSP	GLUCAGON	PRECURSOR (FR	3	
	7	109	39.5	122	Н	GLU2_LOPAM	GLUCAGON	-	r)	
	œ	108	38.8	99	Н	GLUC_ONCKI	GLUCAGON	PRECURSOR (FR	σ	
	σ	108	38.8	121	Н	GLUC_CARAU	GLUCAGON	PRECURSOR,	σ	
. 1	10	106	38.1	59	۲	GLUC_SCYCA	GLUCAGON.		2.07e-05	
-1'	7	104	37.4	124	Н	GLU1_LOPAM	GLUCAGON	I PRECURSOR.	4.72e-05	
-('	12	104	37.4	158	Н	GLUC_PIG	GLUCAGON	PRECURSOR (FR	4	
-1	13	104	37.4	180	,-1	GLUC_BOVIN	GLUCAGON	PRECURSOR.	4.72e-05	
. '	74	104	37.4	180	Н	GLUC_MESAU	GLUCAGON	PRECURSOR.	4.72e-05	
	15	104	37.4	180	~	GLUC_MOUSE	GLUCAGON	PRECURSOR.	4.72e-05	
	9	104	37.4	180		GLUC_OCIDE	GLUCAGON	PRECURSOR,	4.72e-05	
. 1	17	104	37.4	180	Н	GLUC_HUMAN	GLUCAGON	PRECURSOR.	4.72e-05	
	18	104	37.4	180	-	GLUC_CAVPO	GLUCAGON	PRECURSOR.	4.72e-05	
. 1	5	107	37.4	180	-	GLUC_RAT	GLUCAGON	PRECURSOR.	4.72e-05	
	S 1	103	37.1	151	_	GLUC_CHICK	GLUCAGON	PRECURSOR.	7.11e-05	
. •	17	100	36.0	29	-	GLUC_CHIBR	GLUCAGON.		2.40e-04	
. •	77	9	35.6	29	Н	GLUC_TORMA	GLUCAGON.		3.58e-04	
. 1	23	96	34.5	96	1	GLUC_MYOSC	GLUCAGON PRECURSOR	PRECURSOR (FR	1.18e-03	

1.75e-03 2.58e-03	2.58e-03	1.21e-02	1.21e-02	1.21e-02	1.77e-02	2.57e-02	2.57e-02	5.43e-02	7.86e-02	1.13e-01	1.13e-01	4.79e-01	1.93e+00	1.93e + 00	1.93e+00	1.93e+00	1.93e+00	2.71e+00	2.71e+00	2.71e+00
GLUCAGON,	GLUCAGON I.	GLUCAGON.	GLUCAGON.	GLUCAGON PRECURSOR (FR	GLUCAGON PRECURSOR (FR	RNA POLYMERASE BETA SU	RNA POLYMERASE BETA SU	GLUCAGON.	GLUCAGON.	GLUCAGON.	HYPOTHETICAL 47.8 KD P	TYPE II PROTEINS GERAN	EUKARYOTIC TRANSLATION	EUKARYOTIC TRANSLATION	INHIBITOR OF APOPTOSIS	EXCINDCLEASE ABC SUBUN	HYPOTHETICAL PROTEIN M	GASTRIC INHIBITORY POL	UREA TRANSPORTER, ERYT	INHIBITOR OF APOPTOSIS
GLUC_PLAFE GLUZ ORENI	GLU1 ORENI	GLUC_CALMI	GLUC_RABIT	GLUC_CANFA	GLUC_AMICA	RRPL_RABVS	RRPL_RABVP	GLUC_DIDMA	GLUC_ANAPL	GLUC_HYDCO	YBDN_ECOLI	BET4_YEAST	IF5_RAT	IF5_HUMAN	IAP_CHICK	UVRB_HELPY	Y124_METJA	GIP_HUMAN	UT1_HUMAN	IAP1_MOUSE
	Н	М	Н	Н	Н	Н	Н	1	н	Н	Н	ч	Н	Н	ч	Н	Н	Н	Н	Н
3.9	36	29	29	69	75	2127	2142	29	29	36	406	290	429	431	611	658	1075	153	389	900
34.2	33.8	32.4	32.4	32.4	32.0	31.7	31.7	30.9	30.6	30.2	30.2	28.8	27.3	27.3	27.3	27.3	27.3	27.0	27.0	27.0
95	94	06	06	06	8	88	88	86	85	84	84	80	16	76	16	76	76	75	75	75
22 25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	SQUAMATA;	-p.; ic Y. INTERACTS	; 1. Gabs		squamata;
	01-FEB-1991 (REL. 17, CREATED) 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE) 01-FEB-1991 (REL. 22, LAST ANNOTATION UPDATE) 01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE) EXENDIN-3. EXENDIN-3. EUKAROTA, METALOM (MEXICAN BEADED LIZARD). SUKARYOTA, METALOM, VERTEBRATA; LEPIDOSAURIA, SCLEROGLOSSA, ANGUIMORPHA; HELODERMATUDAE; HELODERMA.	SEQUENCE. IISSUE-VENOM; MEDLINE; 91056067. ENG J., ANDREW P.C., KLEINMAN W.A., SINGH L., RAUFMAN JP. ENG J., ANDREW P.C., KLEINMAN W.A., SINGH L., RAUFMAN JP. ENG J., ANDREW P.C., KLEINMAN W.A., SINGH L., RAUFMAN JP. ENG J. G. CHEM. 265:20259-20262(1990). -!- FUNCTION: HAS A VIP/SECRETIN-LIKE BIOLOGICAL ACTIVITY. WITH THE EXENDIN RECEPTOR!- SIMILIARITY: BELONGS TO THE GLUCAGON FAMILY. PIR, A23674; HWG132. PIRS, A23674; HWG132. PIRS, A23674; HMG132.	; Length 39; 38; 0: Indels	4 3 3	IDOSAURIA;
39 AA.	UPDATE) N UPDATE BEADED RATA; LE	SINGH L. in-3, a horridu . E BIOLOG	N. DATION. 98FD3 CRC32; e 260; DB 1; NO. 7.01e-38 Mismatches	PSSGAPPP 	JPDATE) N UPDATE RATA; LE
PRT;	CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE) RIDUM (MEXICAN BEADED I ORDATA; VERTEBRATA; LEF	SUENCE. SSUE-VERNOM; SUINE; 91056067. JUINE; 9105607. JUINE; 910	DATIO AMII ABSI SCOL		, CREATED) , LAST SEQUENCE UPDATE) , LAST ANNOTATION UPDATE) (GILA MONSTER). CHORDATA; VERTEBRATA; LEF
STANDARD;	17, CREATED) 17, LAST SEC 22, LAST ANN M HORRIDUM (MA) A, CHORDATA; ULMORPHA; HEI	JENCE. JUNE; 91056067. JUNE; 9105607.	1GCN. 1K; VENOM; AMI 39 39 1AA; 4204 MW; 93.5%; arity 97.5%; Conservative	LSKOMEEEAVRU 	
	1 (REL. 2 (REL. 2 (REL. HORRIDUM METAZOS	OM; 1056067 DREW P. 10n and ue isol HEM. 26 ON: HAS REITY: B 4; HWGH	11274; 1GCN. ** FAMILY; VE 39 ** A5; ** S A A A5; ** S A A5; *	F-TSDLS 	12 (REL. 22, 18 (REL. 36, 18 (REL. 36, 19 (REL. 36, PRECURSOR. SUSPECTUM (Q METAZOA; CI
лг 1 EXE3_нЕСНО	01-FEB-1991 (REL. 17, CREATED) 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE) 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE) 01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE) EXENDIN-3. HELODERMA HORRIDUM HORRIDUM (MEXICAN BEADED LIZARD). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAUR SCLEROGELOSSA; ANGUIMORPHA; HELODERWATUDAE; HELODERMA	[1] SEQUENCE. TISSUB-VENOM; MEDLINE; 91056067. ENG J., ANDREW P.C., KLEJ PULIIGATION AND STRUCK J. BIOL. CHEM. 265:20259!- FUNCTION: HAS A VIPK; WITH THE EXEMDIN REGI -!- SIMILARITY: BELONGS J PIR; A23674; HWGH3Z. PIR; A23674; HWGH3Z. PROSITE; PROOLEGO	HSSP; P01274; 1GCN. GLUCAGON FAMILY; VENOM; MOD_RES 39 39 SEQUENCE 39 AA; 4204 QUETY MATCH Best Local Similarity 97: Matches 39; Conservativ	1 1 XE4	01-MAY-1992 (REL. 2; 15-701-1998 (REL. 3) 15-701-1998 (REL.) EXENDIN-4 PRECURSOR HELODERMA SUSPECTUM EUKARYOTA; METAZOA;
RESULT ID E	800 B B B B B	7	ETT SO SO SO MA	Db QY RESULT ID E	P E E E E E E E E E E E E E E E E E E E

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REPRESENT SERVICE SERV

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GLUCAGON PRECURSOR (FRAGMENT).
ICTALORUS PUNCTATUS (FRAGMENT).
EUKARYOTA; GHANNEL CAFIESH).
EUKARYOTA; METALOA; CHORDARA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; BUTELEOSTEI; OSTARIOPHYSI; SILURIFORMES; ICTALURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 85157536.
ANDREWS P.C., RONNER P.;
"Isolation and structures of glucagon and glucagon-like peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                catish pancreas."

J. BIOL. CHEM. 260:3910-3914(1985).

-I- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVYL.

-I- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

-I- X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH AMERICAN GOOSEFLES SQUENCES.

-I- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

PROSTE; PS01260; GLUCAGON; 2.

PRRAM; PRO0123; hormone2; 2.

HSSP; P01274; 1GCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-PANCREAS;
MEDLINE; 87156787.
HOOSEIN N.M., MARRENHOLZ A.M., ANDREWS P.C., GURD R.S.;
"Biological activities of catfish glucagon and glucagon-like peptide.";
BIOCHEM. BIOPHYS. RES. COMMUN. 143:87-92(1987).
                                                                                                                                                                                                                                                                                         Length 103;
                                                                                                                                                                                                                                                                                   Score 118; DB 1; Length 103
Pred. No. 1.29e-07;
7; Mismatches 7; Indels
                                                                                                                  GLUCAGON-36 (OXYNTOMODULIN). GLUCAGON-LIKE PEPTIDE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 117; DB 1; Length 71;
Pred. No. 1.99e-07;
8; Mismatches 6; Indels
                                                                                                                                                                                                    GLUCAGON-LIKE PEPTIDE D43EDFC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLUCAGON-LIKE PEPTIDE.
E -> D (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1986 (REL. 03, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C49ED93A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                39 HADGIF-TSDMSSYLEEKAAKEFVDWLIKGRP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLUCAGON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 HADGIY-ISDVSSYLQEQAAKDFIIWLKSGQP
                                                                                       29 GLI
36 GLI
70 GLI
71
103 GLI
11719 MW; I
                                                                                                                                                                                                                                                                                   42.4%;
ilarity 53.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8173 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.1%;
Matches 17; Conservative
     PFAM; PF00123; hormone2; HSSP; P01274; 1GCN.
                                                             GLUCAGON FAMILY; HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLUCAGON FAMILY; HORMONE
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity '
                                                                                                                                                                                                                           103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38
53
71
71 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
TISSUE-PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLUC_ICTPU
P04093;
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                                                                                                                                         PEPTIDE
NON_CONS
PEPTIDE
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PEPTIDE
PEPTIDE
CONFLICT
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SEQUENCE
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                                                                                                                     PEPTIDE
                                                                                          PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the SAMSE Institute of Bioinformatics and the EMED outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelabs-sib.ch).
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                                                                                                                                                                                                             MEDLINE, 92218

ENG J., KLEINEAN W.A., SINGH L., SINGH G., RAUFMAN J.-P.;

"Isolation and characterization of exendin-4, an exendin-3 analogue,

from Heloderme suspectum venom. Further evidence for an exendin

receptor on dispersed acini from guinea pig pancreas.";

J. BIOL. CHEM. 267:7405(1992).

-!- FUNCTION: GAS A VIP/SECRETIN-LIKE BIOLOGICAL ACTIVITY. INTERACTS

WITH THE EXENDIN RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
NEOBATRACHIA; RANOIDEA; RANIDAE; RANINAE; RANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 88257102.
POLLOCK H.G., HAMILTON J.W., ROUSE J.B., EBNER K.E., RAWITCH A.B.;
"Isolation of peptide hormones from the pancreas of the bullfrog (Rana catesbeiana). Amino acid sequences of pancreatic polypeptide, oxyntomodulin, and two glucagon-like peptides.";
J. BIOL. CHEM. 263:9746-9751(1988).
-- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE BLOOD SUGAR LEVEL.
-!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-!- X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH OTHER SPECIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXENDIN-4.
AMIDATION (G-87 PROVIDE AMIDE GROUP)
6C1A8FD5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 256; DB 1; Length 87; Pred. No. 5.73e-37; 2; Mismatches 0; Indels
                                              SEGUENCE FROM N.A.
CHEN Y.E., DRUCKER D.J.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
SCLEROGLOSSA; ANGUIMORPHA; HELODERMATIDAE; HELODERMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 HGEGTF-TSULSKOMEEEAVRLFIEWLKNGGPSSGAPPPS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 3
GLUC_RANCA STANDARD; PRT; 103 AA.
61D(21318); P15439; P15440;
01-APR-1990 (REL. 14, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
GLUCAGON PRECURSOR (FRAGMENTS).
RANA CATESBELANA (BULL FROG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLUCAGON FAMILY; VENOM; AMIDATION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A42486; HWGH4G,
PROSITE; PS00250; GLUCAGON; 1.
PFAM; PF00123; hormone2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; B28091; GCFGB.
PROSITE; PS00250; GLUCAGON; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 AA; 9479 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 92.1%;
Best Local Similarity 92.5%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U77613; G1916067; -.
                                                                                                                                                                    SEQUENCE OF 48-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IISSUE-PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCES
                                                                                                                                                                                           TISSUE-VENOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
SEQUENCE
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P09566;
01-MAR-1989 (REL. 10, CREATED)
01-NOV-1990 (REL. 12, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 28, LAST ANNOFATION UPDATE)
GLUCAGON PRECURSOR (FRAGMENT).
LEPISOSTEUS SPATULA (ALLIGADAR); (ATRACTOSTEUS SPATULA).
SEMIONOTIFORMES; LEPISOSTEIDAE; LEPISOSTEUS.
                                                                                                                                                                                                                                                                                                                                 ANGUILLA ANGUILLA (EOROPEAN FRESHWATER EEL), AND
ANGUILLA ROSTRATA (AMERICAN EEL).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation and structures of alligator gar (Lepisosteus spatula) insulin and pancreatic polypeptide."; GEN. COMP. BUDGCRINGL. 67:375-382(1987).
-!- FUNCTION: PROWDERS HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.
-!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE, 914006B.
MEDINE, 914006B.
MEDINE, 914006B.
TISSUE-PRICERS;
The primary structure of glucagon-like peptide but not insulin has been conserved between the American eel, Anguilla rostrata and the European eel, Anguilla anguilla.";
GEN. COMP. ENDOCRINOL. 82:23-32(1991).
-! SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation of alligator gar (Lepisosteus spatula) glucagon, oxyntomodulin, and glucagon-like peptide: amino acid sequences of oxyntomodulin and glucagon-like peptide: ", mino acid sequences of GEN. COMP. ENDOCRINOL. 69:133-140(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 88030594.
POLLOCK H.G., KIMMEL J.R., HAMILTON J.W., ROUSE J.B., EBNER K.E.,
LANCE V., RAWITCH A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 88196798.
POLLOCK H.G., KIMMEL J.R., EBNER K.E., HAMILTON J.W., ROUSE J.B.
LANCE V., RAWITCH A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEOSTEI; ANGUILLIFORMES; ANGUILLIDAE; ANGUILLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 110; DB 1;
Pred. No. 3.91e-06;
                                                                                               P41521;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
GLUCAGON-LIKE PEPTIDE (GLP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27E8C37D CRC32;
                                                       30 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HAEGIY-TSDVSSYLQDQAAKEFVSWLKTG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION
                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; B61125; B61125.
PIR; C61125, C61125.
PROSITE; PS00260; GLUCAGON; 1.
PFAM: PF00123; hormone2; 1.
HSSP; P01274; 1GCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY SEQUENCE OF 1-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 AA; 3376 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLUCAGON FAMILY; AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 43.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-36 AND 45-78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-PANCREAS;
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RESULT 5

D GLUM_ANGAN
AC 01-NOV-1995
DT 01-NOV-1995
DT 01-NOV-1995
DT 01-NOV-1995
DE GLUCAGON-LIK
OS ANGULILA ROS
OC EUKARYOTA; M
(1)
RP SEQUENCE
RR TSSUE-PANCR
RR TSSUE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KESULT ID GILD OF COLUMN TO COLUMN T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOPHIUS AMERICANUS (AMERICAN GOOSEFISH) (ANGLERFISH).
BUKARYOTA, METALOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PARACANTHOPTERYGII; LOPHIIFORMES; LOPHIIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
THE BLOOD SUGAR LEVEL.
-i- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-i- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROCESSING.
MEDLINE; 86286913.
NOE B.D., ANDREWS P.C.;
Specific glucagon-related peptides isolated from anglerfish islets are metabolic cleavage products of (pre)proglucagon-II.";
PEPTIDES 7:331-339(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LUND P.K., GOODMAN R.H., MONTMINY M.R., DEE P.C., HABENER J.F.; "Anglerfish islet pre-proglucagon II. Nucleotide and corresponding amino acid sequence of the CDNA."; J. BIOL. CHEM. 258:3280-3284(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRPP (GLICENTINE RELATED POLYPEPTIDE).
GLUCAGON II.
; DFEG3061 CRC32;
X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH AMERICAN GOOSEFISH SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                             Length 78;
                                                                                                                                                                                                                                                                             GLUCAGON-36 (OXYNTOMODULIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                            GLUCAGON-LIKE PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 3.91e-06;
9; Mismatches 6;
                                                             -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
PIR; S06339; GCGXA.
PROSITE; PS00260; GLUCAGON; 2.
PREM; PF00123; hormone2; 2.
PRSP; P01274; 1GCN.
                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1986 (REL. 03, CREATED)
01-NOV-1986 (REL. 03, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                     509ED9D3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 AA
                                                                                                                                                                                                                                                                                                                                                                                                Score 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 HADGTY-TSDVSSYLQDQAAKKFVTWLKQG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A05150; GCAF2.
PROSITES, PSOOSE0; GLUCAGON; 2.
PFAM: PF00123; hormone2; 2.
HSSP; P01274; 1GCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 AA; 14171 MW;
                                                                                                                                                                                                                                                                                                                                        78 AA; 8990 MW;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 39.6%;
Best Local Similarity 46.7%;
Matches 14; Conservative
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                                                                                                                                                                                                                  GLUCAGON FAMILY; HORMONE PEPTIDE 1 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; V00632; G64022; -
EMBL; J00933; G213353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1986 (REL. 03,
15-DEC-1998 (REL. 37,
GLUCAGON II PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 83135785.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDE
PEPTIDE
SEQUENCE
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            SS SS REAL RESERVENCES
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PFAM:
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GLOCONCKI STANDARD; PRT; 68 AA.

PO7449;

01-APR-1988 (REL. 07, CREATED)

01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)

01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)

GLUCAGON PRECURSOR (FRAGMENT).

ONCORHYNCHUS KISUTCH (COHO SALMON).

EUKARYOTA; METAZOA; GLORDATA; VERTEBRATA; ACTINOPTERYGII; RELEOSTEI; EUTELEOSTEI; PROTRACANTHOPTERYGII; SALMONIFORMES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
CYPRINIDAE; CYPRININAE; CARASSIUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucagon and glucagon-like peptide.";
REGUL PEPT 14:57-67(1986).
-!- FUNCTION: PROMOTES HYROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
THE BLOOD SUGAR LEVEL.
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 86234328.
PLISETSKAYA E., POLLOCK H.G., ROUSE J.B., HAMILTON J.W., KIMMEL J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-!- X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH AMERICAN
GOOSEFISH SEQUENCES.
-!- GLN-L4 IS A UNIQUE SUBSTITUTION FROM LEUCINE IN OTHER KNOWN
GLUCAGON SEQUENCES AND GLUCAGON-LIKE PEPTIDES.
-!- SIMILARITY: BELONGS TO THE GLUCAGON PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Isolation and structures of coho salmon (Oncorhynchus kisutch)
                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                       Length 122;
                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 108; DB 1; Length 68;
Pred. No. 9.03e-06;
11; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YUEN T.I.H., MOK P.Y., CHOW B.K.C.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLUCAGON-LIKE PEPTIDE.
                Score 109; DB 1; 1
Pred. No. 5.95e-06;
9; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402B55D1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AA
                                                                                                                                      89 HADGTY-TSDVSSYLQDQAAKDFVSWLKAG 117
                                                                                                                                                                              38 HADGTY-TSNVSTYLQDQAAKDFVSWLKSG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLUCAGON.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTR: JP0103: GCONC.
PROSITE: PS00250; GLUCAGON; 2.
PFAM; PF00123; hormone2; 2.
HSSP: P01274; IGCN.
GLUCAGON FAMILY; HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7810 MW;
          Query Match
Best Local Similarity 46.7%;
Matches 14; Conservative
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Best Local Similarity 43.3%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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68
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P79695;
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PEPTIDE
PEPTIDE
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SEQUENCE
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                                                                                                                                                                                                                                                                         PROSITE; PS00260; GLUCAGON; 2.
PFAM; PF00123; hormone2; 2.
HSSP; P01274; IGCN.
GLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.
-!- FUNCTION: PROMOTES HYDROLYSIS OF GLICOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.
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MEDIANGREAS;

MEDIANGREAS;

MEDIANGREAS;

MEDIANGREAS;

MEDIANGREAS;

Primary structure of glucagon from the gut of the common dogfish (scyliorhinus canicula).;

FEBS LETT. 214:50-56(1987).

IF UNDUCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.

IN DESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          GRPP (GLICENTINE RELATED POLYPEPTIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCYLIORHINUS CANICULA (SPOTTED DOGFISH) (SPOTTED CATSHARK).
EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; CHONDRICHTHYES;
ELASMOBRANCHII; CARCHARHINIFORMES; SCYLIORHINIDAE; SCYLIORHINGS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.8%; Score 108; DB 1; Length 121; 43.8%; Pred. No. 9.03e-06; ative 10; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 106; DB 1; Length 29;
Pred. No. 2.07e-05;
7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                               -! - SIMILARITY: BELONGS TO THE GLUCAGON FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-JAN-1990 (REL. 13, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8CFE41FB CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 HAEGTY-TSDISSFLRDQAAQNEVAWLKSGQP 118
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| hsdgtfitsdlskgmeeeavrlfiewlkn 29
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ilarity 51.7%;
Conservative
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50
88
121 AA;
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hes 15; Conserv
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es 14; Conser
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PROSITE; PS00260;
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P09687;
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GLU1_LOPAM
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PEPTIDE
SEQUENCE
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Matches
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Matches
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NATURE 257:751-757 (1975).

-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
-!- FUNCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
-!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-!- X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BUHL I., THIM L., KOFOD H., ORSKOV C., HARLING H., HOLST J.J.; "Naturally occurring products of proglucagon 111-160 in the porcine and human small intestine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SASANI K., DOCKERILL S., ADAMIAK D.A., TICKLE I.J., BLUNDELL T.L., "X-ray analysis of glucagon and its relationship to receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRPP (GLICENTINE RELATED POLYPEPTIDE)
                                                                                                                                                                                                                                                                              SEQUENCE OF 33-61.
BROMER W.W., SINN L.G., BEHRENS O.K.;
The amino acid sequence of glucagon. V. Location of amide groups, acid degradation studies and summary of sequential evidence.";
J. AM. CHEM. SOC. 79:2807-2810(1957).
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 89327238.
ORSKOV C., BERSANI M., JOHNSEN A.H., HOEJRUP P., HOLST J.J.;
"Complete sequences of glucagon-like peptide-1 from human and pig
small intestine.";
GCG.
SUS SCROFA (PIG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLUCAGON FAMILY: HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; 3D-STRUCTURE.

NON_TER 1 30 GRPP (GLICENTINE RELATED POLYPEP PEPTIDE 3 61 GLUCAGON.
PEPTIDE 78 107 GLUCAGON-LIKE PEPTIDE 1.
PEPTIDE 126 158 GLUCAGON-LIKE PEPTIDE 2.
                                                                                                  THIN L., MODY A.J.;
THIN L., MODY A.J.;
"The primary structure of porcine glicentin (proglucagon).";
REGUL. PEPT. 2:139-150(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 37.4%; Score 104; DB 1; Length 158; Similarity 50.0%; Pred. No. 4.72e-05; 15; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                  "The amino acid sequence of porcine glicentin.";
PEPTIDES 2 SUPPL. 2:37-39(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18212 MW; 9FBC1BFE CRC32;
                                             ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 HAEGTF-TSDVSSYLEGQAAKEFIAWLVKG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. BIOL. CHEM. 264:12826-12829(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. BIOL. CHEM. 263:8621-8624(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB; 1GCN; 30-SEP-83.
PROSITE; PS00260; GLUCAGON; 3.
PFAM; PF00123; hormone2; 3.
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107
107
158
452
553
                                                                                                                                                                                                 MEDLINE; 82221776.
THIM L., MOODY A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE OF 111-158.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 78-107.
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Matches 15; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 88243712.
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PDB; 1GCN; 30-SEP
PROSITE; PS00260;
                                                                                                MEDLINE; 81248172
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126
139
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                                                                                  SEQUENCE.
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                                                             GLUCAGON I PRECURSOR.

LOPHIUS AMERICANUS (AMERICAN GOOSEFISH) (ANGLERFISH).

LOPHIUS AMERICANUS (AMERICAN GOOSEFISH) (ANGLERFISH).

EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, ACTINOPTERYGII; NEOPTERYGII;

TELESSTEI; BUTELEOSTEI; PARACANTHOPTERYGII; LOPHIIFORMES; LOPHIIDAE;

LOPHIUS.
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE: 89064585.

NICHOLS R., LEE T.D., ANDREWS P.C.;
PURCTEALLY proglucagon processing: isolation and structures of glucagon and glucagon peptide from gene I.";
ENDOCRINOLOGY 123:2639-2645(1988).
-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.
-!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.
                                                                                                                                                                                                 JUND P.K., GOODMAN R.H., DEE P.C., HABENER J.F.; Pancreatic preproglucagon cDNA contains two glucagon-related coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                MEDLINE; 81215615.
LUND P.K., GOODMAN R.H., HABENER J.F.;
"Pancreatic pre-proglucagons are encoded by two separate mRNAs.";
J. BIOL. CHEM. 256:6515-6518(1981).
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GLUCAGON-LIKE PEPTIDE I.
                                                                                                                                                                                                                                  sequences arranged in tandem.";
PROC. NATL. ACAD. SCI. U.S.A. 79:345-349(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 GRPP (GLICENTINE B
81 GLUCAGON I.
124 GLUCAGON-LIKE PEP:
14165 MW; F2AlDCDA CRC32;
              21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (REL. 01, CREATED) 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) GLUCAGON PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 AA
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EMBL; V00932; G213351; -.
PIR; A01543; GCAF.
PIR; S06458; S06458.
PROSITE; PS00260; GLUCAGON; 2.
PFAM; PF00123; hormone2; 2.
HSSP; P01274; 1GCN.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 53-81 AND 91-124.
MEDLINE; 89064585.
                                                                                                                                                                                                                                                                                    51-83 FROM N.A.
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                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 82197492.
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91
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                                                                                                                                                                                                 LUND P.K.,
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AC P01224.

PDT 21-JUL-1981

DT 01-NV-1991

DI 15-DEC-1999

UI GLUCAGON PI
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PEPTIDE
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TISSUE-PANCREATIC ISLETS;
MEDLINE; 9547722.
ROTHENBERG M.E., ELLERTSON C.D., KLEIN K., ZHOU Y., LINBERG I.,
MCDONALD J.K., MACKIN R.B., NOE B.D.;
MCDONALD J.K., MACKIN R.B., NOE B.D.;
"Processing of mouse proglucagen by recombinant prohormone convertase
1 and immunopurified prohormone convertase 2 in vitro.";
J. BIOL. CHEM. 270:10136-10146(1995).
-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPLIDS, AND RAISES
-!- INDUCTION: PRODUCES HYDROLYSIS OF GLYCOGEN AND LIPLIDS, AND RAISES
-!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
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-:- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                     MEDIINE; 83167563.
BELL G.I., SANTERRE R.F., MULLENBACH G.T.;
"Hamster preproglucagon contains the sequence of glucagon and two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
     SUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALLA; EUTHERLA;
RODENTIA; SCIUROGNATHI; MURIDAE; CRICETINAE; MESOCRICETUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 104; DB 1; Length 180;
Pred. No. 4.72e-05;
7; Mismatches 7; Indels
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GLUCAGON-LIKE PEPTIDE 2.
126ABD83 CRC32;
                                                                                                                                                                                                                                                                                                         BELL G.I.;
SUBMITTED (XXX-1985) TO EMBL/GENBANK/DDBJ DATA BANKS.
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01-0cT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-UL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR.
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20954 MW;
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PFAM; PF00123; hormone2; 3.
HSSP; P01274; 1GCN.
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Best Local Similarity 50.0%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          THE BLOOD SUGAR LEVEL.
                                                                                                                                                                                           related peptides.";
NATURE 302:716-718(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J00059; G305354; -.
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92
146
180 AA;
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PROSITE; PS00260;
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SEQUENCE FROM N.A.
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P55095;
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SEQUENCE
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BROMER W.W., BOUCHER M.E., KOFFENBERGER J.E. JR.;

"Amino acid sequence of bovine glucagon.";

J. BIOL. CHEM. 246:2822-2827(1971).

-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
THE BLOOD SUGAR LEVEL.

THE BLOOD SUGAR LEVEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOPEZ L.C., FRAZIER M.L., SU C.-J., KUMAR A., SAUNDERS G.F.; "Mammalian pancreatic preproglucagon contains three glucagon-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOYOIDEA; BOYIDAE; BOSINAE; BOS
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Pred. No. 4.72e-05;
7; Mismatches 7; Indels
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34640341 CRC32;
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                         (REL. 33, LAST SEQUENCE UPDATE) (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                           180 AA.
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13-AUG-1987 (REL. 05, LAST SEQ
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ilarity 50.0%;
Conservative
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HSSP; P01274; 1GCN.
                                                                                                             STANDARD;
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GLUC_BOVIN
P01272;
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P01273;
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LOPEZ L.C
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- ! - SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

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EMBL; 246845; G59981; -.

EMBL; 246845; G59981; -.

EMBL; 246845; G59981; -.

EMBL; 246845; GCG.

BW SIMILARITY.

FPAM; PPO0123; hormone2; 3.

GIUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.

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Search completed: Mon Oct 4 15:29:03 1999 Job time : θ secs.

98 HAEGTF-TSDVSSYLEGQAAKEFIAWLVKG 126 |::|| || :| || :| || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :|

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Mon Oct 4 15:29:20 1999; MasPar time 6.45 Seconds 338,430 Million cell updates/sec MPsrch_pp Run on:

>MOHAM-312-CLAIM83A.PEP (1-40) from moham312177.pep 1 hsdgtfitsdlskqmeeeavrlfiewlknggpssgappps 40 Description:
Perfect Score:
Sequence:

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PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1.sp_archea 2.sp_bacteria 3.sp_fung1 4.sp_human
1.sp_arches
5.sp_invertebrate 6.sp_mammal 7.sp_mhc 8.sp_organelle
9.sp_phage 10.sp_hant 11.sp_rodent 12.sp_unclassified
13.sp_vertebrate 14.sp_virus

Mean 34.509; Variance 61.367; scale 0.562 Statistics:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.67e-12	2.38e-11	1.03e-05	1.03e-05	1.03e-05	1.03e-05	1.03e-05	2.42e-04	1.13e-03	1.13e-03	5.09e-03	2.24e-02	1.36e-01	2.74e-01	5.50e-01	7.75e-01	1.09e+00	1.53e+00	2.14e+00	2.99e+00	
Description	PROGLUCAGON I.	PROGLUCAGON II.	GLUCAGON (FRAGMENT).	PROGLUCAGON (FRAGMENT)	PROGLUCAGON (FRAGMENT)	GLUCAGON I.	GLUCAGON II.	PROGLUCAGON.	PROGLUCAGON.	PROGLUCAGON.	L PROTEIN, RNA DEPENDE	HYPOTHETICAL 42.3 KD P	REPLICASE.	APOLIPOPROTEIN N-ACYLT	HYPOTHETICAL 151.9 KD	UDP-GLUCOSE 4-EPIMERAS	ACETYL COA CARBOXYLASE	T25B9.7 PROTEIN.	HYPOTHETICAL 95.1 KD P	HYPOTHETICAL 35.4 KD P	
А	042143	042144	091188	091409	091408	091971	091189	091410	012955	012956	057294	085863	038064	067000	055359	059082	012721	022770	023629	55625	10004
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Length DB	266	219	99	72	72	178	178	206	149	204	2127	379	552	439	1319	338	2185	502	44	200	9
A Query Match	52.9	51.1	6.68	39.9	39.9	39.9	39.9	37.1	35.6	35.6	34.2	32.7	30.9	30.2	29.5	29.1	8 8	28.6	200		7
Score	147	142	111	111	111	111	111	103	000	5	95	16	86	84	82	8 6	C	0 6	σ,	7 (
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2.99e+00 4.16e+00 4.16e+00 4.16e+00 4.16e+00 4.16e+00 5.77e+00 5.77e+00 5.77e+00 5.77e+00 5.77e+00 7.98e+00 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01
FILAMENT-A PRECURSOR. 115. 300AA LONG HYPOTHETICA INTEGRASE/RECOMBINASE. IAP HOMOLOG. HYPOTHETICAL 77.8 KD P NITRITE REDUCTASE (EC PROTEIN-TROSINE PHOSP YEMJ PROTEIN. ADENYLLY-SULPHATE REDU PEPTIDYLARGININE DEIMI ROSHS. 4 PROTEIN. MEDIUM-CHAIN ACYL-COA HYPOTHETICAL 18.1 KD P C33ELO. 8 PROTEIN. PUTALIVE VIRAL IEGUMEN CARBOXYPEPTIDASE. WINGED HELLY PROTEIN. FORMATE DEHYDROGENASE 1352AB LONG HYPOTHETIC NEURORASCIN PRECURSOR.
P70868 080115 069151 069151 067319 007319 007319 007319 0021764 0021764 0021764 0021764 001798 001798 001798 001798 001798
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ALIGNMENTS

		ANURA;	.,	with		Gaps			anura;
PRT; 266 AA.	CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE)	ATA; AMPHIBIA; BATRACHIA; OPODINAE; XENOPUS.	SEQUENCE FROM N.A. MEDILINE; 97368292. IRWIN D.M., SATKUNARAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A.,	WHEELER M.B.; "The Xenopus proglucagon gene encodes novel GLP-1-like peptides with insulinctropic properties."; PROC. NATL. AAD. SCI. U.S.A. 94:7915-7920(1997).	E6139A25 CRC32;	Score 147; DB 13; Length 266; Pred. No. 2.67e-12; 8; Mismatches 5; Indels 1;	WLINGGPS 128 wlknggps 33	PRI; 219 AA. CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE)	XENOPUS LAEVIS (AFRICAN CLAWED FROG). EURARYOTA, METAZOA, CHORDATA, VERTEBRATA, AMPHIBIA; BATRACHIA; ANURA; MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS. SEQUENCE FROM N.A.
PRELIMINARY; P	(TREMBLREL. 05, CREAT (TREMBLREL. 05, LAST (TREMBLREL. 08, LAST	PROGLUCASON I. XENOPUS LAEVIS (AFRICAN CLAMED FROG). EUKRAKOTR, METAZOA; CHORDATA; VERTEBR MESOBATRACHIA; PIPOIDEA; PIPIDAE; XEN	INARAJAH M., WE	WHEELER M.B.; "The Xenopus proglucagon gene einsulinctropic properties."; PROC. NATL. ACAD. SCI. U.S.A. 5	EMBL; AFU0443.5; GZ3020.0; T. PROSITE; PS00260; GLUCAGON; S. PFRAF; PF00123; hormone2; S. SEQUENCE 266 AA; 30951 MW;	52.9%; 57.6%; rative	HAEGTF-ISDVIQQLDEKAAKEFIDWLINGGPS :: :	PRELIMINARY; i (TREMBLREL. 05, CRI (TREMBLREL. 05, LAN (TREMBLREL. 08, LAN	XENOPUS LAEVIS (AFRICAN CLAWED FROS). EURARYOTA, METAZOA, CHORDATA, VERTEBR MESOBATRACHIA, PIPOIDEA, PIPIDAE, XEN [1] SEQUENCE FROM N.A.
PRELI		GON I. LAEVIS (A A; METAZO ACHIA; PI	[1] SEQUENCE FROM N.A. MEDLINE; 97368292. IRWIN D.M., SATKUN	M.B.; lopus prog tropic pr	004432; G PS00260; 00123; hc	similarity 19; Conserv	SGTF-TSDV7 : :: gtfitsdle		LAEVIS (AF TA; METAZOA RACHIA; PIP E FROM N.A.
O42143	01-JAN-1998 01-JAN-1998 01-JAN-1998 01-NOV-1998	PROGLUCAGON XENOPUS LAE EUKARYOTA;] MESOBATRACH	[1] SEQUENCE MEDLINE; IRWIN D.N	WHEELER M.B.; "The Xenopus I insulinotropic PROC. NATL. AC	EMBL; AF PROSITE; PFAM; PF SEQUENCE	Query Match Best Local Matches	97 HAI : : 1 hsc	ESULT 2 ID 042144 AC 042144; DT 01-JAN-1998 DT 01-JAN-1998 DT 01-NOV-1998 DE PROGLUCAGON	XENOPUS I EUKARYOTA MESOBATRA [1] SEQUENCE
RESULT ID O	2555	S S S S	rr RX RA	RR RE	80 DR 80	ō m ×	da Qy	RESI ID AC DI DI	00 00 RN RP

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PFAM; PF00123; hormone2; 2.
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271102; 201232;

01-NOV-1996 (TREMBLREL. 01, CREATED)

01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

01-NOV-1998 (TREMBLREL.)

PROGLUCAGON (FRAGMENT)

ONCORHYNCHUS TSCHAMMYTSCHA (CHINOOK SALMON) (KING SALMON).

BUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; BUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;

ONCORHYNCHUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL. 01, LAST ANDOTATION UPDATE)
01-NOV-1998 (TREMBLREL. NEOPIERYGII; SALMONIDAE;
01-NOV-1996 (TREMBLREL. 01, LAST ANDOTATION UPDAE)
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MEDLINE, 95295739.
MEDLINE, 95295739.
Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
MOL. ENDOCRINOL. 9:267-277(1995).
EMBL: S78474: E206590; -.
EMBL: 919920; G736367; -.
                                                                     "The Xenopus proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties."; PROC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997).
EMBL; AF004433; G2305018; -. PROSITE; PS00260; GUUSON; 3. PROMIN: PF00123; hormone2; 4. SEQUENCE 219 AA; 25271 MW; 45C42A88 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRWIN D.M., WONG J.;
"Trout and chicken proglucagon: alternative splicing generates mRNA
"Transcripts encoding glucagon-like peptide 2.";
KDE ENDOCRINOL. 9:267-277(1995).
EMBL: U19913; G736361; ...
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                   MEDLINE; 97368292.
IRMIN D.M., SATKUNARAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A.,
WHEELER M.B.;
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                                                                                                                                                                                                                                                           Query Match
51.1%; Score 142; DB 13; Length 219;
Best Local Similarity 51.5%; Pred. No. 2.38e-11;
Matches 17; Conservative 10; Mismatches 5; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 111; DB 13; Length 66;
Pred. No. 1.03e-05;
10; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 66 AA; 7680 MW; 62C576E2 CRC32;
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                                                                                                                                                                                                                                                                                                                                                           97 HAEGIF-ISDVIQHLDEKAAKEFIDWLINGGPI 128
                                                                                                                                                                                                                                                                                                                                                                                        33 HADGTY-TSDVSTYLQDQAAKDFVSWLKSG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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st Local Similarity 46.7%;
tches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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MEDLINE; 95295739.
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Q91188
Q91188;
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EUKARYOTA; METAZOA; CHORDATA; VERIEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PROGLOCAGON (FRAGMENT)
PROGLOCAGON (FRAGMENT)
ONCORHYNCHUS WIXISS (RAI)
EUGRAYOCHS, METAROA, CHORDATA, VERTEBRATA, ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE; 95295739.
ITROUT and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
MOL. ENDOCRINOL. 9:267-277(1995).
EMBL; 878473; G999383; -
PFAM; PF00123; hormone2; 2.
NON_TER 72 72
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"TRWIN D.M., WONG J.;
"Trout and chicken proglucagon: alternative splicing generates mRNA
"Transcripts encoding glucagon-like peptide 2.";
MOL. BNDCRINOL. 9:267-277(1995).
BABL: 019917, 673-6355;
BRBL: S78475; 6999385;
PROSITE; PS00.260; GLUCAGON; 3.
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Pred. No. 1.03e-05;
10; Mismatches 5; Indels
                                         Length 72;
                                                                                     Indels
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                      Score 111; DB 13; L
Pred. No. 1.03e-05;
10; Mismatches 5;
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OF7AF3EC CRC32;
                                                                                                                                                                                                                                                                             72 AA.
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                                                                                                                                     39 HADGTY-TSDVSTYLQDQAAKDFVSWLKSG
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TISSUE-INTESTINE, DISTAL PORTION;
MEDLINE; 95295739.
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Best Local Similarity 46.7%;
Matches 14; Conservative
72 AA; 8293 MW;
                                           39.9%;
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                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                             PRELIMINARY;
                                              Query Match
Best Local Similarity
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Matches

g ð 091189

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SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES; RHABDOVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HELODERMA SUSPECTUM (GILA MONSTER).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAURIA; SQUAMATA;
SCLEROGLOSSA; ANGUIMORPHA; HELODERMATIDAE; HELODERMA.
                                                                                                                                                                  HELODERMA SUSPECTUM (GILA MONSTER).
BUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAURIA; SQUAMATA;
SCLEROGLOSSA; ANGUIMORPHA; HELODERMATIDAE; HELODERMA.
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larity 50.0%; Pred. No. 1.13e-03;
Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 99; DB 13; Length 149
Pred. No. 1.13e-03;
6; Mismatches 8; Indels
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01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
L PROTEIN, RNA DEPENDENT RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PROGLUCAGON.
                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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17224 MW; F763AB51 CRC32;
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                149 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRI;
                   PRT;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
CHEN Y.E., DROCKER D.J.;
J. BLOD., CHEM. 0:0-0(0).
EMBL; U77611; G1916063; -.
PROSITE; PS00260; GLUCAGON; 1.
PPAM: PF00123; hormone2; 2.
SEQUENCE 149 AA; 17224 MW; F'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
CHEN Y.E., DRUCKER D.J.;
J. BIOL. CHEM. 0:0-0(0).
EMBL: U77612; G1916065; -.
PROSITE; $500260; GLUCAGON; 2.
                                                                04,00
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Best Local Similarity 50.0%;
Matches 15; Conservative
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                     PRELIMINARY;
                                                         01-JUL-1997 (TREMBLREL. 01-JUL-1997 (TREMBLREL. 01-NOV-1998 (TREMBLREL. PROGLUCAGON.
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MINAMOTO N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RABIES VIRUS
VIRUSES; SSR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYSSAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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057294
057294;
JLT 9
012955
012955;
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                                                                                                                                                                                                  Q91189; Q92168;
Q91189; Q92168;
Q1 NOV-1996 (TREMBLREL. 01, CREATED)
O1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
O1-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GLUCAGON II.
EUROCRAFINGTHS MYKISS (RAINDOW TROUT) (SALMO GAIRDNERI).
EURARYOTA: METAZOA: CHORDATA, VERTEBRATA; ACTINOPTERYGII; TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUB-INTESTINE, DISTAL PORTION;
MEDLINE: 95295739.
IRWIN D.M., WONG J.;
Transcripts encoding plucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.7;
MOL. ENDOCRINOL. 9:267-277(1995).
EMBL, 019916; G736372;
EMBL, 019915; G736372;
UNPOLE: 019916; G736372;
UNED.
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
              ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
              Indels
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 1.03e-05;
10; Mismatches 5;
                .;
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U19915; G736371; -.
PF00123; hormone2; 3.
NCE 178 AA; 19998 MW; A4299C13 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
                   10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 HADGTY-TSDVSTYLQDQAAKDFVSWLKSG 118
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                                                                                        PRT;
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08,
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Best Local Similarity 46.7%;
Matches 14; Conservative
                       Conservative
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 95295739.
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                       14;
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TABATA S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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SECURICE FROM N.A.
STRAIN-F199;
STRAIN-F199;
STRAIN-F199;
SENSIN G.W.; GAASTERLAND I., SAFFER J.D., FREDRICKSON J.K.;
SENSEN C.W.; GAASTERLAND I., SAFFER J.D., FREDRICKSON J.K.;
"Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromaticivorins strain F199.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF079317; G3378295; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; LEVIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; ZYMOMONAS GROUP;
                                                                                                                                                                                                                                                                                                                                  Score 95; DB 14; Length 2127; Pred. No. 5.09e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 91; DB 2; Length 379;
Pred. No. 2.24e-02;
9; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                 SUBMITTED (JAM-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, ABO09663; D1024994; -.
EMBL, ABO09661; D1024989; -.
SEQUENCE 2127 AA; 242427 WW; 847321FB CRG32;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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08, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL PROTEIN; PLASMID.
SEQUENCE 378 AA; 42269 MW; ED0127FC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 A.A.
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skqmeeeavrlflewlknggpssgappps 40
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01-NOY-1998 (TREMBLREL. 08, LAST SEQI
01-NOY-1998 (TREMBLREL. 08, LAST SEQI
01-NOY-1998 (TREMBLREL. 08, LAST ANW
HYPOTHETICAL 42.3 KD PROTEIN.
SPHINGOMONAS AROMATICIVORANS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Q38064 PRELIMINARY;
Q1-NOV-1996 (TREMBLREL. 01, CR
Q1-NOV-1996 (TREMBLREL. 01, LA
Q1-NOV-1998 (TREMBLREL. 08, LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57
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EMBL; X80191; G517241; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.7%;
Best Local Simil:rity 37.9%;
atches 11; Conservative
                                                                                                                                                                                                                                                                                                                                             Query Match 34.2%;
Best Local Similarity 47.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 NLNSPLIEDPVRLMLEWLKTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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BACTERIOPHAGE PP7
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPHINGOMONAS
                                                                                                           STRAIN-RC-HL;
                                                                                                                                 MINAMOTO N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEVIVIRUS.
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085863
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DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEER R., SNEAD M.A., KELLER M., AUJAY M., HUBER R., FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex accidens";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   괊
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. sequence features in the 1Mb region from map positions 64% to 92% of the genome."; DNA RES. 2:153-166(1995).
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 96127529.
KANEKO T., TANAKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N., SUGIUKA M., TABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-VF5;
DECKERT G., WARREN P.V., GRASTERLAND T., YOUNG W.G., LENOX A.L.,
DECKERT G., WARREN P.V., SNRAD M.A., KELLER M., AUJAY M., HUBER I
FELDMAN R.A., OLSON G.J., SWANSON R.V.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AE000709; G2983774; -
TRANSFERASE; ACYLTRANSFERASE; LIPOPROTEIN.
SEQUENCE 439 AA; 50757 MW; 79632D20 CRC32;
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                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 439;
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                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
HYPOTHETICAL 151.9 KD PROTEIN.
SYNECHOCYSTIS SP. (STRAIN PCC 6803).
                                                                                                                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
. No. 1.36e-01;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 30.2%; Score 84; DB 2; L Best Local Similarity 35.1%; Pred. No. 2.74e-01; Matches 13; Conservative 10; Mismatches 13
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                                                                                                                                                                                                                                                                                                                                                BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1319 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 sdgtfitsdlskqmeeeavrlfiewlknggpssgapp
                                                                                                                                                                                     439 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
                                                                                                                                                                                                                         01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQ
01-NOV-1998 (TREMBLREL. 08, LAST ANN
                                                                                                                                                                                     PRT;
  Best Local Similarity 45.0%; Pred.
Matches 9; Conservative 9; A
                                                                                                                                                                                                                                                                                    APOLIPOPROTEIN N-ACYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7. 15 PRELIMINARY;
Q55359 CS5359 COL-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
                                                                                  |:||:::| || :::||:|
10 dlskqmeeeavrlfiewlkn 29
                                                               483 DISKRLDDE-VR-YVDWLRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NATURE 392:353-358(1998).
                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               AQUIFEX AEOLICUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-PCC6803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-PCC6803;
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RC STRAIN-PCC6803;

RX MEDLINE; 97061201.

RA ANDLINE; 97061201.

RA ANTALIMA N., HIROSARA M., SUGIURA M., SASAMIZU E., NAKAMURA Y.,

RA MINALIMA N., HIROSARA M., SUGIURA M., SASAMOTO S., KIMURA T.,

RA MINALIMA N., HIROSARA M., SUGIURA M., SASAMOTO S., KIMURA T.,

RA HIROS S., TAKEUCHI C., WADA T., WARAZAKI N., NARDO K., OKUMURA S.,

RA TABARA S.;

RT ARABAS S.;

RY Sequence analysis of the genome of the unicellular cyanobacterium

RT Synechocyasis sp. PCC6803. II. Sequence determination of the entire

RT Synechocyasis sp. PCC6803. II. Sequence determination of the entire

RT Synechocyasis sp. PCC6803. II. Sequence determination of the entire

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RT Synechocyasis sp. PCC6803. II. Sequence determination of the entire

RT Synechocyasis sp. PCC6803. II. Sequence determination of the entire

RM HYPOTHETICAL PROTEIN.

RW HYPOTHETICAL PROTEIN.

SQ SEQUENCE 1319 AA: 151893 MW; EB2F4ACB CRC32;

QUELY MATCH

SQ SEQUENCE 1319 AA: 151893 MW; CS SOGE 01;

Best Local Similarity 34.6%; Pred. NO. 5.50e-01;

MATCHES 9; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
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Search completed: Mon Oct 4 15:29:34 1999

g

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 13.75 Seconds 61.875 Million cell updates/sec Mon Oct 4 15:32:14 1999; : עט עוים

not generated. Tabular output

1 hgegtfitsdlskgmeeeavrlfiewlknggpssgappps 40 >MOHAM-312-CLAIM83B.PEP (1-40) from moham312177.pep 281 Description: Ferfect Score: Sequence: tle:

GF 80

claim X1X2 = 1

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

a-geneseg35 Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part1 8:part12 13:part13 8:part14 15:part19 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part28 24:part24 22:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 33:part33 33:part33 33:part39 39:part39

Variance 106.235; scale 0.238 Mean 25.274; Statistics: pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	1.02e-15	1.02e-15	1.02e-15	1.02e-15	4./4e-15	4.74e-15	4.74e-15	2.40e-13	1.18e-11	2.79e-11	1.56e-10	1.56e-10	6.96e-10	2.02e-09	3.09e-09	3.096-09
	Description	Exendin-4, for use in	Heloderma suspectum e	Gila monster exendin-	Heloderma suspectum p	Heloderma horridum ex	Exendin-3, for use in	Gila monster exendin-	Leu(14), Phe(25)-exen	Heloderma suspectum e	Heloderma suspectum e	Exendin-4 (1-30) for	Heloderma suspectum e	H. horridum exendin-4	H. horridum exendin-4	Exendin-4 (1-28) amid	H. horridum exendin-3
	GI (I	W61770	R80546	W47609	W70288	R80545	W61769	W47608	W61773	R80547	R80543	W61771	R80544	W39302	W39309	W61772	W39301
	DB	100	7	30	3	14	6	30	3.6	14	14	33	74	53	59	39	5 3
	Query Match Length DB	08	000) M	87	39	6 6	000	0.00	31	31	30	31	30	30	28	30
æ	Query	02.6	9 4	9.60	93.6	16	1. [6	1.1.5	7 7 7 7	7.00	76.9	74.0	74.0	71.5	8.69	69.0	69.0
	Score	263	200	2 6	263	256	250	27.0	2000	220	216	208	208	201	961	194	194
- Anna Anna Anna Anna Anna Anna Anna Ann	Result No.	1	4 (4 "	o ◀	· ur	א נ	7 0	- 00	00	101	: =	12	1.	7	15	16

3.09e-09	23e-0	23e-0	736-C	73e-C	946-0	10e-c	10e-C	3/e-0	000	0.000	226	596-1	0.96-	0.96-	0.96-0	58e-(58e-(586-	586-	Tae-	- 98T	. 18e-	.18e-	.18e-	.18e-	186	9 6	, 700
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194	190	190	190	190	0 0	0 00	188	187	186	186	186	2 6	200	η τ Ο α Ο α	יו מ לי	184	701	184	184	* C) (F	7 6	0 0	0 0	TAR	183	183	182
17	0 0	16	, c	22	9 6	9 6	4 C	25	27	00	000) C	2 6	10	9 6	0 0	* ¥	י ע מי מי	ה ה	0	0 0	n (* •	4.	7.4	43	44	45

ALIGNMENTS

07-JAN-1997; US-035404.

R 08-AGG-1997; US-055404.

R 08-AGG-1997; US-055404.

R NO-1997; US-055404.

R NO-1997; US-055404.

R AMYL-) AMYLIN PHARM INC.

Reclay NRA, Bhavaar S, Prickett KS;

Relegy NRA, Bhavaar S, Prickett KS;

RPI; 98-398796/34.

R PT; 98-398796/24.

R PT; 98-386796/26.

R PT; 98-388796/26.

R PT; 98-38876/26.

R PT; 98-388796/26.

R PT; 98-388796/26.

R PT; 98-388796/26.

R PT; 98-388796 Exendin-4, for use in treating disorders related to food intake. Exendin; obesity; type II diabetes; eating disorders; cardiac disease; insulin resistance syndrome; elevated plasma glucose level; agonist. Heloderma suspectum. RESULT 1 ID W61770 standard; peptide; 39 AA. 29-MAR-1999 (first entry) 16-JUL-1998. 07-JAN-1998; U00449. 14-NOV-1997; US-066029. 07-JAN-1997; US-034905. WO9830233

Gaps 1; 93.6%; Score 263; DB 39; Length 39; larity 97.5%; Pred. No. 1.02e-15; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 39; Conserv

1;

hgegtf-tsdlskqmeeeavrlfiewlknggpssgappps 39

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1 hgegtfitsdlskgmeeeavrlfiewlknggpssgappps 40

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Stimulating/inhibiting insulin release with exendin polypeptide(s) - for treating diabetes mellitus and preventing hyperglycaemia.
Claim 6; Columns 13-14; 17pp; English.
R80546 is Heloderma suspectum exendin-4. It is an insulinotropic peptide, and can therefore be used in the treatment of diabetes mellitus (types I or II), and for the prevention of hyperglycaemia. It normalises hyperglycaemia through glucose-dependent and insulin-(in) dependent mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Regulating gastrointestinal motility using exendins or their Regulating gastrointestinal motility using exendins or their agonists - for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations claims 20 and 21; Fig 1; 70pp; English.

#47549 describes a generic exendin agonist, provided that it does have the formula of either exendin-3 (#47608) or exendin-4 (#47609).
                                                                    Heloderma suspectum exendin-4.
Exendin-4; diabetes mellitus; hyperglycaemia; insulinotropic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exendin agonists, which reduce gastric motility and delay gastric emptying, can be used to treat spasm (where associated with acute diverticulitis or disorders of the billary tract or sphincter of oddi), postprandial dumping syndrome and hyperglycaemia oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type I diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. They can also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic resonance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gila monster exendin-4.

Exendin agonis: gastric motility; gastric emptying; treatment;
Exendin agonis: gastric motility; gastric emptying; treatment;
Exendin agonis: gastric motility; gastric postprandial hyperglycaemia;
type I diabetes; impaired glucose tolerance; toxin ingestion;
obesity; Gila monster venom; exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 263; DB 14; Length 39;
Pred. No. 1.02e-15;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hgegtf-tsdlskqmeeeavrlfiewlknggpssgappps 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beeley NRA, Gedulin B, Prickett KS, Young AA;
WPI; 98-145351/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W47609 standard; peptide; 39 AA.
                 R80546 standard; peptide; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.6%;
ilarity 97.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUL-1998 (first entry)
                                                         27-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-FEB-1998,
08-AUG-1997; U14199,
08-AUG-1996; US-694954,
(AMYL-) AMYLIN PHARM INC
                                                                                                                                                                     24-MAY-1993; 056480.
24-MAY-1993; US-066480.
(ENGJ/) ENG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heloderma suspectum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                   Heloderma suspectum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                             US5424286-A.
                                                                                                                                                                13-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W47609;
                                                                                                                                                                                                                                             Eng J;
WPI; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
KWEDTA
                                                                                                                                                                                                                                                                                                          #3388888
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New Possible V33163.

New nucleic acid encoding proexendin - used to diagnose and treat, new nucleic acid encoding proexendin - used to diagnose and treat, new nucleic acid encoding protection to treat poisoning by reptile venomery e.g. endocrine tumours, also to treat poisoning by reptile venomery claim 3: Fig 2: 26pp; English.

The Heloderma suspectum proexendin peptide is encoded by its cDNA which was isolated from all will suspectum salivary gland cDNA library. The proexendin protein comprises of a novel exendin N-terminal peptide (ENTP) linked to the N-terminus of the exendin A peptide peptide contains of the exendin Proexendin con a ldentify related sequences (e.g. the conding agency defects associated with metabolic disease) and species of the proexendin peptide can be used to raise antibodies. Anti-proexendin peptide can be used to raise antibodies. Anti-proexendin with altered levels of proexendin (e.g. endocrine tumours and organ antibodies are claimed to be useful for diagnosing conditions associated with altered levels of proexendin (e.g. endocrine tumours and organ failure), for identifying other regulators of cell metabolism, in drug squence 87 AA;

Sequence 87 AA;
                                                                                                                                                                                                                                                                                                     Heloderma suspectum proexendin peptide.
Heloderma suspectum proexendin; exendin N-terminal peptide; ENTP;
exendin 4 peptide; exendin 3 gene; Heloderma horridum; metabolic disease;
drug screening; endocrine tumour; organ failure; cell metabolism;
diabetes; reptilian venom peptide.
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                                                                                                                                  Gaps
 Exendins, components of Gila monster venom, have some sequence similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and pervention of hyperglycaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                   Length 39;
                                                                                                                                  Indels
                                                                          Score 263; DB 30; Len
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Pred. No. 1.02e-15;
0: Mismatches 0;
                                                                                                                                                                  1 hgegtf-tsdlskgmeeeavrlfiewlknggpssgappps 39
                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              1..23
/note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Exendin 4"
                                                                                                                                                                                                                                                                W70288 standard; Protein; 87 AA.
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Local Similarity 97.5%;
Les 39; Conservative
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(ONEO-) 1149336 ONTARIO INC
                                                                                                     h
Similarity 97.5%;
39; Conservative
                                                                                                                                                                                                                                                                                                 (first entry)
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04-FEB-1998; CA0071.
07-FEB-1997; GB-002582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..47
/note=
48..87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                             Heloderma suspectum.
                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-1997;
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                                                                                                                                                                                                                                                                                                 06-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                      W70288;
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Gaps

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RESULT

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W61773;
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17-JUL-1998.
17-JUL-1997; US-056029.
18-NOV-1997; US-034905.
18-NOV-1997; US-034905.
18-NOV-1997; US-034405.
18-NOV-1997; US-055440.
18-N
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With the standard of the s
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Exendin-3, for use in treating disorders related to food intake.
Exendin: obesity: type II diabetes: eating disorders: cardiac disease;
Exendin: obesity: type II elevated plasma glucose level: agonist.
                                                                                   Heloderma horridum exendin-3.
Exendin-3; diabetes mellitus; hyperglycaemia; insulinotropic peptide.
Heloderma horridum.
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pred. No. 4.74e-15;
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Pred. No. 4.74e-15;
2; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n 6
W61769 standard; peptide; 39 AA.
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Best Local Similarity 92.5%;
Matches 37; Conservative
T
R80545 standard; peptide; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Conservative
                                                                       (first entry)
                                                                                                                                                                                                                             24-MAY-1993; 066480.
24-MAY-1993; US-066480.
(ENGJ/) ENG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heloderma horridum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compounds for use
Sequence 39 AA;
                                                                       -FEB-1996
                                                                                                                                                                                       US5424286-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W61769;
                                                                                                                                                                                                                                                                                                                            Eng J;
WPI; 9
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Gaps

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Indels

hsdgtf-tsdlskqmeeeavrlflewlknggpssgappps 39

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Exendin; obesity; type II diabetes; eating disorders; cardiac disease;
Insulin resistance syndrome; elevated plasma glucose level; agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Regulating gastrointestinal motility using exendins or their agonists for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations claims 20 and 21; Fig 1; 70pp; English.

W447549 describes a generic exendin agonist, provided that it does have the formula of either exendin-3 (W47608) or exendin-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exendin agonists, which reduce gastric motility and delay gastric Exendin agonists, can be used to treat spasm (where associated with acute emptying, can be used to treat spasm (where associated with acute oldiverticulitis or disorders of the biliary tract or sphincter of oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type I diabetes, imparised glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. They can also be administered to subjects undergoing gastrointestinal diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exendins, components of Gila monster venom, have some sequence similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   investigation, particularly radiological or by magnetic resonance
                                                                                                    Exendin agonist; gastric motility; gastric emptying; treatment; spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type i diabetes; impaired glucose tolerance; toxin ingestion; obesity; Gila monster venom; exendin-3.
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-4 No. 4.74e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-AUG-1996; US-694954.
(AMYL-) AMYLIN PHREM INC.
BENEY NRA, Gedulin B, Prickett KS, Young AA;
WPI; 98-145351/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                  Location/Qualifiers
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W61773 standard; peptide; 39 AA.
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Best Local Similarity 92.5%;
Matches 37; Conservative
RESULT 7
TD W47608 standard; peptide; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-1999 (first entry)
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JAN-1998; U00449.
14-NOV-1997; US-066029.
07-JAN-1997; US-034905.
                                                                                         Gila monster exendin-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heloderma suspectum.
                                                                                                                                                                                                                                                                                                                                           12-FEB-1998,
08-AUG-1997; U14199.
                                                                                                                                                                                                                     Heloderma horridum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified_site
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                                                                                                                                                                                                                                                                   Modified_site
                                                                                                                                                                                                                                                                                                                    W09805351-A1
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                                                                     03-JUL-1998
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29-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JAN-1997; US-034905;
08-AUG-1997; US-055404.
14-NOV-1997; US-065442.
                                                                                                                                                                                                                                                                                                                                                                       Heloderma suspectum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JAN-1998; U00449
14-NOV-1997; US-066
                                                                                                                                      31 AA;
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(ENGJ/) ENG J.
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ID R8
AC R8
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                        AMYL-) AMYLIN PHERM IN.

AMYL-) AMYLIN PHERM IN.

Beeley NRA, Bhavsar S, Prickett KS;

Beeley NRA, Bhavsar S, Prickett KS;

Reducing food intake by administering exendins or their

Peducing food intake by administering exendins or their

analogues - for treatment of e.g. obesity, type II diabetes,

analogues - for treatment of e.g. obesity, type II diabetes,

callengates and insulin resistance

car alleviated by reducing food intake, in particular obesity, type

I diabetes, eating disorders, insulin resistance syndrome, elevated

comprises administering an exendin or an exendin agonist. The method

consumption as effectively as amylin or cholecystokinin but has a much

longer-lasting cation (still effective after 6 hours in a mouse model).

The present sequence is that of an exendin-4 variant which is one of

the preferred compounds for use in the method.
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Stímulating/inhibiting insulin release with exendin polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                          27-FED-1996 (first entry)
Heloderma suspectum exendin-4 residues 9-39 (Extendin-4(9-39)).
Exendin-4; residues 9-39; Exendin-4(9-39);
insulinotropic peptides; inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-1996 (first entry)
Reloderma suspectum exendin-4 residues 1-31 (Exendin-4(1-31)).
Exendin-4; residues 1-31; Exendin-4(1-31); diabetes mellitus; hyperglycaemia; insulinotropic peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for treating diabetes mellitus and preventing hyperglycaemia.
claim 7; columns 13-14; 17pp, English.
R80547 is the Heloderma suspectum exendin-4 residues 9-39. It
is an insulinotropic peptide activity inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 220; DB 14; Length 31;
Pred. No. 1.18e-11;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  Score 238; DB 39; Length 39;
Pred. No. 2.40e-13;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                       1 hgegtf-tsdlskgleeeavrlfieflknggpssgappps 39
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R80547 standard; peptide; 31 AA.
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Best Local Similarity 100.0%;
Mulches 31; Conservative
                                                                                                                                                                                                                                                                     Match 84.7%;
Local Similarity 92.5%;
Les 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUN-1995.
24-MAY-1993; 066480.
24-MAY-1993; US-066480.
(ENGJ/) ENG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-1993; 066480.
24-MAY-1993; US-066480.
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USS424286-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heloderma suspectum.
US5424286-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                               R80547;
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                                                                                                                                                                                                                                                                                                   Matches
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Reducing food intake by administering exendins or their analogues - for treatment of e.g. obesity, type II diabetes, analogues - for treatment of e.g. obesity, type II diabetes, cating disorders and insulin resistance cating disorders that a leaves to a new method for treating disorders that the invention relates to a new method for treating disorders that it diabetes, eating disorders, insulin resistance syndrome, elevated plasma glucose levels, or the risk of cardiac disease. The method plasma glucose levels, or the risk of cardiac disease. The method comprises administering an exendin or an exendin agonist. The treatment comprises appetite and lowers plasma lipid levels. It inhibits food consumption as effectively as anylin or cholecystokinin but has a much longer-lasting action (still effective after 6 hours in a mouse model). The present sequence is that of exendin-4 (1-30) or its amide which is one of the preferred compounds for use in the method.
WPI; 95-262627/34.

Stimulating/inhibiting insulin release with exendin polypeptide(s) -
Stimulating/inhibiting and preventing hyperglycaemia.

for treating diabetes mallitus and preventing hyperglycaemia.

Claim 1; Columns 13-14; 17pp; English.

RR0543 is the Heloderma suspectum exendin-4 residues 1-31. It is an
insulinotropic peptide, and can therefore be used in the treatment of
diabetes mellitus (types I or II), and for the prevention of
hyperglycaemia. It normalises hyperglycaemia through glucose-dependent
and insulin-(in)dependent mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exendin-4 (1-30) for use in treating disorders related to food intake. Exendin; obesity; type II diabetes; eating disorders; cardiac disease; insulin resistance syndrome; elevated plasma glucose level; agonist.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "optionally the C-terminal is in amide form"
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                                                                                                                                                                                                                                                                                                                                                                                   Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                   Score 216; DB 14; Length 31 Pred. No. 2.79e-11; 0; Mismatches 0; Indels
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Heloderma suspectum exendin-4 residues 1-31-Tyr31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
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Pred. No. 1.56e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31
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WPI; 98-398796/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        r 11
W61771 standard; peptide; 30 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 96.8%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                               uuery Match 76.9%;
Best Local Similarity 96.9%;
Matches 31; Conservative
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1 hgegtfitsdlskqmeeeavrlfiewlkng 30

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W39309
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                                                                        SOUTH SERVICE STATE OF THE SERVICE STATE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This peptide is a fragment of exendin-4 isolated from Heloderma horridum. This peptide and its salts, esters and derivatives can be wised to treat diabetes mellitus. They stimulate biosynthesis and secretion of insulin, but have the opposite effect on glucagon, and independent of this activity can increase peripheral glucose utilisation. Exendin-3 and exendin-4 are only active when blood sugar levels are high, so they will not induce hypoglycaemia. Compared with glucagon-like peptide I (5LPI) and the known exendins, they are more active (effective at lower doses), more stable to degradation and metabolism and have a longer lasting effect. Truncated forms of this peptide can be made more economically than full length versions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                                                                                                      Stimulating/inhibiting insulin release with exendin polypeptide(s) for treating diabetes mellitus and preventing hyperglycaemia.
Claim 2; Columns 13-14; 17pp; English.
R80544 is the Heloderma suspectum exendin-4 residues 1-31, where the native pro31 has been replaced with a Tyr residue. It is an the native pro31 has been replaced with a Tyr residue. It is an almostropic peptide, and can therefore be used in the treatment of diabetes mellitus (types I or II), and for the prevention of hyperglycaemia. It normalises hyperglycaemia through glucose-dependent and insulin (in) dependent mechanisms.
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13-SEP-1996; EC-037230.

13-SEP-1996; DE-037230.

(BOEF ) BOBHRINGER MANNHEIM GMBH.

(GOEF ) BOCHERINGER MANNHEIM GMBH.

GOEKE B, GOEKE R, Hoffmann E;

Truncated versions of exendin peptide(s) for treating diabetes -

Increase secretion and blosynthesis of insulin, but reduce those of

Juncagon, and do not induce hypoglycaemia

Claim 1; Page 4; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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1. horidum exendin-4 peptide.
Exendin-3: exendin 4: diabetes; insulin; secretion; biosynthesis; glucagon reduction; hypoglycaemia; glucose; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note "This residue can be any amino acid except
Exendin-4: residues 1-31; y-31-Exendin-4(1-31); diabetes mellitus;
hyperglycaemia; Tyr31; insulinotropic peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Pred. No. 1.56e-10;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 hgegtf-tsdlskqmeeeavrlfiewlkngg 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wery Match 74.0%; est Local Similarity 96.8%; alches 30; Conservative
                                                                                                                                                24-MAY-1993; 066480.
24-MAY-1993; US-066480.
(ENGJ/) ENG J.
                                                                  Heloderma suspectum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heloderma horridum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 AA;
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juucagon, and do not induce hypoglycaemia claim 2; Page 22; 150pp; English.

Peptides w39303-w39304.0 are fragments of exendin-3 and exendin-4 peptides w39304.0 are fragments of exendin-3 and exendin-4 peptides w39304.0 are fragments of exendin-3 and exendin are used in a novel method for the treatment of diabetes mellitus. These peptides can stimulate hisosynthesis and secretion of insulin, but have the opposite effect on biosynthesis and secretion of insulin, but have the opposite effect on glucagon, and independent of this activity can increase peripheral glucose utilisation. Exendin-3 and exendin-4 are only active when blood sugar levels are high, so they will not independent. Compared with glucagon-like peptide 1 (GLPI) and the known exendins, they are more active (effective at lower doses), more stable to degradation and metabolism and have a longer lasting effect. Truncated forms of this peptide can be made more economically than full length versions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
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Exendin-4 (1-28) amide for use in treating disorders related to food.
Exendin: obesity: type II dlabetes; eating disorders; cardiac disease;
Exendin: obesity: type II dlabetes; eating disorders; ardiac disease;
insulin resistance syndrome; elevated plasma glucose level; agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rruncated versions of exendin peptide(s) for treating diabetes - increase secretion and biosynthesis of insulin, but reduce those of
                                                                     05-JUN-1998 (first entry)
#1. horridum exendin-4 peptide derivative #6
Exendin-3; exendin 4; diabetes; insulin; secretion; biosynthesis;
glucagon reduction; hypoglycaemia; glucose; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note≈ "the C-terminal is in amide form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 196; DB 29;
Pred. No. 2.02e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                              /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beeley NRA, Bhavsar S, Prickett KS; WPI; 98-398796/34.
                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                   11-DEC-1997.
05-7UN-1997.
05-7UN-1996; DE-037230.
05-JUN-1996; DE-02502.
(BOEF ) BOERRINGER MANNHEIM GMBH.
GOEKE B, GOEKE R, HOLFMANN EY.
WPI; 98-042119/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 15
W61772 standard; peptide; 28 AA.
T 14
W39309 standard; peptide; 30
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Best Local Similarity 93.3%;
Matches 28; Conservative
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07-JAN-1997; US-034905.
08-AUG-1997; US-055404.
14-NOV-1997; US-065442.
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                                                                                                                                                                             Heloderma horridum.
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29-MAR-1999
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Gaps

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The invention relates to a new method for treating disorders that

C are alleviated by reducing food intake, in particular obesity, type

C if diabetes, earling disorders, insulin resistance, elevated

C plasma glucose levels, or the risk of cardiac disease. The method

C comprises administering an exendin or an exendin agonist. The treatment

C reduces appetite and lowers plasma lipid levels. It inhibits food

C consumption as effectively as amylin or cholecystokinin but has a much

C longer-lasting action (still effective after 6 hours in a mouse model).

C The present sequence is that of exendin-4 (1-28) amide which is one of

S Sequence 28 AN;
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Search completed: Mon Oct 4 15:32:30 1999 Job time : 16 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Oct 4 15:31:48 1999; MasPar time 6.27 Seconds 255.433 Million cell updates/sec "abular output not generated. Run on:

>MOHAM-312-CLAIM03B.PEP (1-40) from moham312177.pep 281 1 hgegtfitsdlskqmeeeavrlfiewlknggpssgappps 40 Ltle: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

122810 seqs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 35.094; Variance 64.811; scale 0.541 pir60 1:pir1 2:pir2 3:pir3 4:pir4 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	1.82e-34	4.97e-33	3.26e-06	3.26e-06	7.09e-06	2.25e-05	2.25e-05	3.30e-05	3.30e-05	4.82e-05	4.82e-05	4.82e-05	7.05e-05	1.03e-04	1.50e-04	3.17e-04	3.17e-04	3.17e-04	3.17e-04	3.17e-04	3.17e-04	3.17e-04	3.17e-04	
	Description	exendin-4 - Gila mons	exendin-3 - Mexican b	qlucadon G2 - North A	dlucadon precursor -	precu	ucagon-like	glucagon G1 - North A	-11ke	glucagon-like peptide	glucagon - chinook sa	glucagon II precursor	glucagon I precursor	Б	qlucagon 2 precursor	glucagon precursor -	glucagon - smaller sp	dlucadon precursor -	glucagon precursor -	qlucadon precursor -	qlucagon precursor -	dlucadon precursor -	qlucadon precursor -	glucagon precursor -	
	ΩI	HWGH4G	HWGH3Z	544472	GCFGB	GCIDC	544473	S44471	B61125	C61125	151093	151057	I51058	GCGXA	GCAF2	GCONC	GCDF	GCPG	A57294	GCHY	GCRIDU	CBO	GCGP	GCHU	
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	ength I	39	0 6	3.5	101	1 6	30	31	30	30	99	178	178	72	122	09	29	158	180	180	180	180	0 0 0	180	
ф	Query Match Length DB	93.6) (* * <	404	. 6	50.00	3.6	39.1		0 00	0.00	38.4	38.1	37.7	37.0	0.74	37.0	27.0	0.76	37.0	0.76	37.0	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M. Biochem. J. (1994) 300:339-345
Characterization of insulins and proglucagon-derived peptides From a phylogenetically ancient fish, the paddlefish (Polyodon spathula).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucagon; glucagon-36 (oxyntomodulin); glucagon-like peptide
1; glucagon-like peptide 2
                                                                                                                      Additions are venom components that are thought to bind to receptors Exendins are venom components that are thought to bind to receptors for vasoactive intestinal peptide and/or secretin on pancreatic acinar cells and to activate adenylate cyclase, resulting in secretion of amylase.

TION **superfamily glucagon amidated carboxyl end; duplication; secretagogue; venom amidated carboxyl end; duplication; secretagogue; venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the sequence from Fig. 3 is inconsistent with that from Fig. 5 in having 29-Glu #superfamily glucagon carbohydrate metabolism; duplication; hormone; pancreas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S44472  #type complete
glucagon G2 - North American paddlefish (Polyodon spathula)
#formal_name Polyodon spathula
19-Mar-1997  #sequence_revision 12-Dec-1997  #text_change
20-Mar-1998
#journal J. Biol. Chem. (1990) 265:20259-20262
#title Purification and structure of exendin-3, a new pancreatic
secretagogue isolated from Heloderma horridum venom.
#cross-references WUID:91056067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pollock, H.G.; Hamilton, J.W.; Rouse, J.B.; Ebner, K.E.; Rawitch, A.B.
                                                                                                                                                                                                                                                                         #modified site amidated carboxyl end (Ser) #status
experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *product glucagon G2 *status predicted *label
*length 31 *molecular-weight 3682 *checksum 7826
                                                                                                                                                                                                                                                                                                               #longth 39 #molecular-weight 4204 #checksum 9591
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41.3%; Score 116; DB 2; Length 31;
Best Local Similarity 53.3%; Pred. No. 3.26e-06;
Matches 16; Conservative 7; Mismatches 6; Indels
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31-Mar-1993 #sequence_revision 31-Mar-1993
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glucagon precursor - bullfrog (fragments)
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Pred. No. 4.97e-33;
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B28091; C28091; D28091
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##residues
1-31 ##label NGU
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 92.5%;
Matches 37; Conservative
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                                                                                                       ##molecule_type protein
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glucagon precirsor - channel catfish (fragments)
#formal_name Ictalurus punctatus #common_name channel catfish
31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
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experimental *label G36\
*product glucagon *status predicted *label GCN\
*product glucagon-like peptide 1 *status experimental
*label G11\
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*label GL2
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##residues 30-63 ##label AND2
#IncATION #wuperfamily glucagon
ADS carbohydrate metabolism; duplication; hormone; pancreas
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##residues 69-101 ##label PO3
##residues 69-101 ##label PO3
FFICATION #superfamily glucagon
RPS carbohydrate metabolism; duplication; hormone; pancreas
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#fitle Isolation and structures of glucagon and glucagon-like peptide from catfish pancreas.
              bullfrog (Rana catesbelana). Amino acid sequences of pancreatic polypeptide, oxyntomodulin, and two glucagon-like peptides.

#cross-references MID:88257102
#accession B28091
J. Biol. Chem. (1988) 263:9746-9751 Isolation of peptide hormones from the pancreas of
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Pred. No. 3.26e-06;
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##residues 1-29 ##label AND1
                                                                                                                                                                                                                                ##molecule_type protein
##residues 37-68 ##label POL
                                                                                                                                                                 ##molecule_type protein
##residues 1-36 ##label PO2
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Best Local Similarity 50.0%;
Matches 16; Conservative
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A05166; A05167
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#journal Gen. Comp. Endocrinol. (1991) 82:23-32
#title The primary structure of glucagon-like peptide but not insulin has been conserved between the American eel.
Anguilla rostrata and the European eel, Anguilla anguilla.
#accession B61125
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                                                                                                                                                                                                                                                                       *length 30 *molecular-weight 3376 *checksum
                                                                                                                                                                                                                                                                                                      Score 110; DB 2; Length vv.
Pred. No. 3.30e-05;
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amidated carboxyl end; duplication
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amidated carboxyl end; duplication
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glucagon - chinook salmon
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##residues 1-30 ##label CON
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##molecule_type protein
##molecule_type protein
1-30 ##label CON
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Best Local Similarity 46.7%;
Matches 14; Conservative
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Local Similarity 46.7%;
les 14; Conservative
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Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (Polyodon spathula).
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                                                                                                                                                                   Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M. Biochem. J. (1994) 300:339-345 Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (Polyodon spathula).
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glucagon Gl - North American paddlefish (Polyodon spathula)
#formal_name Polyodon spathula
18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change
20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                      *product glucagon-like peptide *status predicted *label
                                    S44473 #type complete
glucagon-like peptide - North American paddlefish (Polyodon
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#formal_name Anguilla rostrata #common_name American eel
10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change
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FICATION #superfamily glucagon
DS carbohydrate metabolism; duplication; hormone; pancreas
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                                                                                    #formal_name Polyodon spathula
18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change
20-Mar-1998
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*length 31 *molecular-weight 3751 *checksum 7808
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Conlon, J.M.; Andrews, P.C.; Thim, L.; Moon, T.W.
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##residues 1-30 ##label NGU
FFICATION #superfamily glucagon
tDS duplication; hormone; pancreas
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##residues 1-31 ##label NGU
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53.3%;
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Irwin, D.M.; Wong, J.
Mol. Endocrinol. (1995) 9:267-277
Trout and chicken proglucagon: alternative splicing generates
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#label GDP\
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*product glucagon-like peptide *status experimental
                          #modified_site amidated carboxyl end (Arg) #status
predicted
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#journal Mcl. Endocrinol. (1995) 9:267-277
#title Irout and chicken proglucagon: alternative splicing generates
#cross-references MUID:95295739
#cross-references MUID:95295739
#cross-references MUID:95295739
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glucagon I precursor - rainbow trout
#formal_name Oncorhynchus mykiss #common_name rainbow trout
13.5ep-1996 #sequence_revision 13.5ep-1996 #text_change
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glucagon II precursor - rainbow trout
#formal_name Oncorhynchus mykiss #common_name rainbow trout
13-sep-1996 #sequence_revision 13-sep-1996 #text_change
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mRNA transcripts encoding glucagon-like peptide #cross-references MUID:95295739 #accession I51093
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AS5895
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##cross-references EMBL:U19916; NID:g736369; PID:g736372
roession 151038
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                                                    ##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
                                                                                             ##residues 1-66 ##label IRW ##cross-references EMBL:U19920; NID:g736366; PID:g736367 CLASSIFICATION #superfamily glucagon
                                                                                                                                                                                              Score 109; DB 2; Length 66; Pred. No. 4.82e-05; 11; Mismatches 5; Indels
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Mol. Endocrinol. (1995) 9:267-277
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#length 66 #checksum 1440
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| hgegtfitsdlskqmeeeavilflewlkng 30
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##molecule_type mRNA
##racidnes 1-178 ##label IRW
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151057; 151039; 151038
A55895
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Best Local Similarity 43.3%;
Matches 13; Conservative
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oxyntomodulin
glucagon; glucagon-36 (oxyntomodulin); glucagon-like peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #formal_name Lepisosteus spatula #common_name alligator gar. 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #ERENCE SO(6339
#authors Pollock, H.G.; Kimmel, J.R.; Ebner, K.E.; Hamilton, J.W.;
#authors Pollock, H.G.; Kimmel, J.R.; Ebner, K.E.; Hamilton, J.W.;
#soure, J.B.; Lance, V.; Rawitch, A.B.
#soure Comp. Endocrinol. (1988) 69:133-140
Gen. Comp. Endocrinol. (1988) 69:133-140
Isolation of alligator gar (Lepisosteus spatula) glucagon,
#title oxyntomodulin, and glucagon-like peptide.
#cross-references MUID:88196798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type protein
##residues 39-72 ##label PO2

## x's at positions 37-38 represent a pair of basic amino acids

x's at positions 37-38 represent a pair of basic amino acids

forming a cleavage site.

forming a cleavage site.
                                                                                                                                          Gaps
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#superfamily glucagon
duplication
#length 178 #molecular-weight 20034 #checksum 5250
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glucagon precursor - alligator gar (fragment)
                                                               **status preliminary; translated from GB/EMBL/DDBJ
***bolecule_type mRNA
***posid:...
                                                                                                                                                                                                                            preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 'M',114-144 ##label IR4
##cross-references EMBL:U19919; NID:9736374; PID:9736377
-cession I51036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 58-123 ##label IR3
##cross-references EMBL:019913; NID:9736360; PID:9736361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                   #status
##molecule_type nRNA
##residues 52.3,'x',55-123 ##label IR2
##residues 58:S78473; NID:g999382; PID:g999383
##crosr references GB:S78473; NID:g999382; PID:g999383
##crosr references GB:S78473; Translated from GB/EMBL/D
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larity 43.3%; Pred. No. 4.82e-05;
Conservative 11; Mismatches 5;
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##residues 1-36 #*label POL
                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type mRNA
##residues 58-11
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Matches 13; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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glucagon; glucagon-1ike peptide 1
fromal_name Oncorhynchus kisutch #common_name coho salmon 20-sep-1988 #sequence_revision 30-sep-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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glucagon 2 precursor - American goosefish
glucagon; glucagon-like peptide 1
*formal_name Lophius americanus *common_name American
gcosefish
31-Mar-1993 *sequence_revision 31-Mar-1993 *text_change
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Lund, P.K.; Goodman, R.H.; Montminy, M.R.; Dee, P.C.; Habener, J.F. Habener, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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38.4%; Score 108; DB 1; Length 72;
Best Local Similarity 43.3%; Pred. No. 7.05e-05;
Matches 13; Conservative 10; Mismatches 6; Indels
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A94232
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Mon Oct 4 15:30:56 1999; MasPar time 3.31 Seconds . 341.168 Million cell updates/sec MPsrch_pp Run on:

>монди-312-сгатм83в.РEP (1-40) from moham312177.pep 281 1 hgeytfitsdlskqmeeeavrlfiewlknggpssgappps 40 not generated. tle: Description: Perfect Score: Sequence: Tabular output

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot37 1:swissprot Database:

Mean 35.954; Variance 59.615; scale 0.603 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Pred. No.	1.95e-38	7.046-7	3.376-07	70 200 7	0 876-06	0.0.0	4.00 m	7.0000	130-05	130-05 7	0.15610	יים	5.13e-05	5.13e-U5	5.136-05	5.13e-05	5.13e-05	5.13e-05	7.72e-05	1.16e-04	2 870-04	10.00.0	700010	7.100	
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	æ	Query Match I	93.6	91.1	41.3	40.9	39.1	38.4	38.4	38.1	37.7	37.0	37.0	37.0	37.0	37.0	37.0	7.7			1.0	20.1	36.3	35.2	34.5	33.5	
		Score	263	256	116	115	110	108	108	107	106	104	104	104	104	104	104	100	, c	* * C	* C	103	102	66	97	94	
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2.78e-03 4.09e-03	6.01e-03	1.88e-02	1 886-02	2 746-02	70 047.0	20-047.7	20 247.2	20 247.0	20.000.0	1.205.1	1.20e-01	I./3e-UI	5.05e-01	1 020+00	1 020+00	00+077	00+000	001000	2.026700	2.02e+00	2.84e+00	2.846+00	
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ALIGNMENTS

Score 263; DB 1; Length 87; Pred. No. 1.95e-38;

93.68; 97.58;

Query Match Best Local Similarity

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PFAM; PF00123; hormone2; 3. HSSP; P01274; 1GCN. GLUCAGON FAMILY; HORMONE.
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TISSUE-PANCREAS;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
NEOBATRACHIA; RANOIDEA; RANIDAE; RANINAE; RANA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLLOCK H.G., HAMILTON J.W., ROUSE J.B., EBNER K.E., RAWITCH A.B.; "Isolation of peptide hormones from the pancreas of the builfrog (Rana catesbeluna). Amino acid sequences of pancreatic polypeptide, oxyntomodulin, and two glucagon-like peptides."; J. BIOL. CHEM. 263:9746-9731(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-!- X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH OTHER SPECIES
                                                                                                                                                                                                                                                                                            J. BIOL. CHEM. 255:20259-20262(1990).

-! FUNCTION: HAS A VIP/SECRETIN-LIKE BIOLOGICAL ACTIVITY. INTERACTS
HITH THE EXENDIN RECEPTOR.
-! STMILARITY: BELONGS TO THE GLUCAGON FAMILY.

PIR: A23674; HWGH3Z.
TWGSTIE; PSO1260; GLUCAGON; 1.
FRSP; P01274; LGCN.
GLUCAGON FAMILY: VENOM: AMIDATION.
GLUCAGON FAMILY: VENOM: AMIDATION.
SEQUENCE 39 AA; 4204 MW; AB598FD3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
      Gaps
                                                                                                                                                                     HELODERMA HORRIDUM HORRIDUM (MEXICAN BEADED LIZARD).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAURIA; SQUAMATA;
SCLEROGLOSSA; ANGUIMORPHA; HELODERMATIDAE; HELODERWA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ϊ;
      ï
                                                                                                                                                                                                                                   TISSUE-VENOM;
MEDILINE; 91056067.

FIG. J., ANDREW P.C., KLEINMAN W.A., SINGH L., RAUFMAN J.-P.
FIG. J., ANDREW P.C., KLEINMAN W.A., SINGH L., RAUFMAN J.-P.
FIG. J., ANDREW P.C., KLEINMAN W.A., SINGH L., RAUFMAN J.-P.
FIG. J., ANDREW P.C., KLEINMAN W.A., SINGH L., RAUFMAN J.-P.
Secretagogue isolated from Heloderma horridum venom.";
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 HSDGTF-TSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS 39
       ó
                                         48 HGEGTF-TSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
91.1%; Score 256; DB 1; 3
Best Local Similarity 92.5%; Pred. No. 7.64e-37;
Matches 37; Conservative 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
PIR; B28091; GCFGB.
PROSITE; PS00260; GLUCAGON; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLUC_RANCA STANDARD; PRT; 103 AA. P15438; P15439; P15440; 01-APR-1990 (REL. 14, CREATED) 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE) GLUCAGON PRECURSOR (FRAGMENTS).
                                                                                                                           01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
        0; Mismatches
                                                                                                     39 A.A.
                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE BLOOD SUGAR LEVEL.
        Conservative
                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 88257102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCES
        39;
                                                                                                     EXE3_HELHO
P20394;
                                                                                                                                                                EXENDIN-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                            SEQUENCE
          Matches
                                                                                           RESULT
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ICTALDURUS PUNCTATUS (CHANNEL CATFISH).
EUKARYOTA; METAZOA; CHORDALA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; SILURIFORMES; ICTALURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 85157536.
ANDREWS P.C., RONNER P.;
"Isolation and structures of glucagon and glucagon-like peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. BIOL. CHEM. 260:3910-3914(1985).
-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN THE SERONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-1- X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH AMERICAN GOOSETISHS SEQUENCES.
-1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
PROSITE; PROSIDE, GLUCAGON; 2.
PREAM; PRO0123; hormone2; 2.
HSSP; P01274; 1GCN.
GLUCAGON FAMILY; HORMONE.
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOOSEIN N.M., MAHRENHOLZ A.M., ANDREWS P.C., GURD R.S.; *Biological activities of catfish glucagon and glucagon-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 115, DB 1; Length 71;
Pred. No. 5.17e-07;
9; Mismatches 6; Indels
                                                                                                                     Score 116; DB 1; Length 103.
Pred. No. 3.37e-07;
...___thes 7; Indels
                                                                                                                                       Length 103;
GLUCAGON.
GLUCAGON-36 (OXYNTOMODULIN).
                                       GLUCAGON-LIKE PEPTIDE 1.
                                                                          GLUCAGON-LIKE PEPTIDE 2.
D43EDFC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLUCAGON-LIKE PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E -> D (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IOCHEM. BIOPHYS. RES COMMUN. 143:87-92(1987).
                                                                                                                                                                                                                                                                                                                                                                         01.NOV-1986 (REL. 03, CREATED)
01-WAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C49ED93A CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 HADGTY-TSDVSSYLQEQAAKDFITWLKSGQP 68
                                                                                                                                                                                                                                                                                                                                         71
                                                                                                                                                                                                                                                        32
                                                                                                                                                                                                                   39 HADGIF-ISDMSSYLEEKAAKEFVDWLIKGRP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLUCAGON
                                                                                                                                                                                                                                          29 GLC
36 GLC
70 GLA
71 GLA
11719 MW; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8173 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.9%;
50.0%;
                                                                                                                                       h 41.3%;
Similarity 50.0%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                                                                                                                                                         STANDARD;
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71
53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catfish pancreas.",
                                                                                                  103 AA;
                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-PANCREAS;
MEDLINE; 87156787.
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-!- X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH AMERICAN GOOSDEISH SEQUENCES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P04092;
01-NOV-1986 (REL. 03, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSIDE: PS00260; GLUCAGON; 2. PFAM; PF00123; hormone2; 2. HSSP; P01274; 1GCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
13527 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

Best Local Similarity 46.9%;
Matches 15; Conservative
                                                                                                                                                                                         1 29
1 36
45 78
78 AA; 8990 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U65528; G1762777; -.
                                                                                                                                                                                                                                                                                              38.4%;
Best Local Similarity 43.3%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                    GLUCAGON FAMILY; HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
50
88
121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLUCAGON PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLU2_LOPAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLUC_CARAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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PEPTIDE
PEPTIDE
                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                  PEPTIDE
PEPTIDE
                                                                                                                                                                                              PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEPISOSTEUS SPATULA (ALLIGATÓR GAR) (ATRACTOSTEUS SPATULA).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
SEMIONOTIFORMES; LEPISOSTEIDAE; LEPISOSTEUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLICOR W. G., KIMMEL J.R., HAMILTON J.W., ROUSE J.B., EBNER K.E., LANCE V., RAWITCH A.B.;
Insolation and structures of alligator gar (Lepisosteus spatula) insulin and pancreatic polypeptide.";
GEN. COMP. ENDOCRINOL. 67:375-382(1987).
-:- FUNCTION: PROMOTES HYDROLYSIS OF GIXCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.
-:- FUNCTION: PROMOTES HYDROLYSIS OF GIXCOGEN AND LIPIDS, AND RAISES IN THE BLOOD SUGAR LEVEL.
-:- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
                                                                                GLUM_ANGAN STANDARD; PRT; 30 AA.
P4152I.
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST NNOTATION UPDATE)
ANGUILLA ROSTEATA (BARRICAN PEL). AND
ANGUILLA ROSTEATA (AMERICAN PEL). ANGUILLA ROSTEATA (AMERICAN PEL).
EUKARYOTA METAZOA. CHORDARATA VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; ANGUILLIFORMES; ANGUILLIDAE; ANGUILLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                       TISSUB-PANCREAS;
MEDLINE; 91340068.
CONDON J.W.;
CONDON J.W., ANDREWS P.C., THIM L., MOON T.W.;
Chief primary structure of glucagon-like peptide but not insulin has been conserved between the American eel, Anguilla rostrata and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation of alligator gar (Lepisosteus spatula) glucagon, oxyntomodulin, and glucagon-like peptide: amino acid sequences of oxyntomodulin and glucagon-like peptide."; GEN. COMP. ENDOCRINOL. 69:133-140(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-PANCREAS;
MEDLINE: 88196798.
POLLOCK H.G., KIMMEL J.R., EBNER K.E., HAMILION J.W., ROUSE J.B.
LANCE V., RAWITCH A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          score 110; DB 1; Length 30;
Pred. No. 4.29e-06;
....matrhes 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          European eel, Anguilla anguilla.";
GEN. COMP. ENDOCRINOL. 82:23-32(1991).
-! SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
PIR. B61125; B61125.
PIR.; C61125; C61125.
PROSITE: PS00260; GLUCAGON; 1.
PFAM: PFO0123; hormone2; 1.
HSSP; P01274; 1GCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (REL. 10, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27E8C37D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 AA
                                                                             30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HAEGTY-TSDVSSYLQDQAAKEFVSWLKTG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY SEQUENCE OF 1-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLUCAGON PRECURSOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 AA; 3376 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-36 AND 45-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLUCAGON FAMILY; AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 46.7%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-PANCREAS;
MEDLINE; 88030594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLUC_LEPSP
P09566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT TO GLODE OF THE SULT OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
CYPRINIDAE; CYPRININAE; CARASSIUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

YUEN T.T.H., MOK P.Y., CHOW B.K.C.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

ITE PUNCTION: PROMOTES HIDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.

-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRPP (GLICENTINE RELATED POLYPEPTIDE). GLUCAGON. GLUCAGON-LIKE PEPTIDE. DDB662CE CRC32;
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
                                                                                                                                                                                                                                                                                                                                                              Ϊ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 108; DB 1; Length 121; Pred. No. 9.87e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                       Length 78;
                                                                                                                                                                                              GLUCAGON-36 (OXYNTOMODULIN)
GLUCAGON-LIKE PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                          Score 108; DB 1; 1
Pred. No. 9.87e-06;
10; Mismatches 6
-i- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
PIR; S06339; GCGXA.
PROSITE: PS00260; GLUCAGON; 2.
PERM: PF00123; hormone2; 2.
HSSP; P01274; IGCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches
                                                                                                                                                                                                                                                        509ED9D3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 AA.
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158 AA.
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| hgegtfitsdlskqmeeeavrlfiewlkn 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLUCAGON.
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29
68
68
7810 MW;
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larity 51.7%;
Conservative
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llarity 40.0%;
Conservative
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nes 12; Conser
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les 15; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 AA;
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P09687;
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ID GLUC_PIG
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PEPTIDE
PEPTIDE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lb.ch).
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GLUCAGON PRECURSOR (FRAGMENT).
ONCORHYNCHUS KISUTCH (COHO SALON).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTSLEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES;
                                              LOPHIUS AMERICANUS (AMERICAN GOOSEFISH) (ANGLERFISH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII; TELEOSTEI; EUTELEOSTEI; PARACANTHOPTERYGII; LOPHIIFORMES; LOPHIIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 86234328.
PLISETSKAYA E., POLLOCK H.G., ROUSE J.B., HAMILTON J.W., KINMEL J.R.,
GORBMAN A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PS02560; GLUCAGON: 2.
PFAM; PF001274; LGCN.
GLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE: 86286913.

NOE B.D., ANDREWS P.C.;

NOE B.D., ANDREWS P.C.;

"Specific glucagon-related peptides isolated from anglerfish islets
"Specific glucagon-related peptides isolated from anglerfish islets
are metabolic cleavage products of (pre)proglucagon-II.";

PEPTIDES 7:331-339(1986).

-1- FUNCTION: PROMOTES HYRROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES

-1- FUNCTION: PROMOTED IN THE A CELLS OF THE ISLETS OF LANGERHANS

IN RESPONSE TO A DROP IN BLOOD SUGAR CONCEMPRATION.

-1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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GLUCAGON II.
GLUCAGON-LIKE PEPTIDE II.
; DFE63061 CRC32;
                                                                                                                                                                                                                                                                      LUND P.K., GOODMAN R.H., MONTMINY M.R., DEE P.C., HABENER J.F., "Anglerfish is let pre-proglucagon II. Nucleotide and corresponding amino acid sequence of the cDNA.";
J. BIOL. CHEM. 258:3280-3284(1983).
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Pred. No. 1.49e-05;
....matches 6; Indels
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01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
U1-NOV-1986 (REL. 03, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUCAGON II PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.1%;
Best Local Similarity 43.3%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; V00632; G64022; -
EMBL; J00933; G213353;
PIR; A05150; GCAF2.
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52
89
122 AA;
                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 83135785.
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EUGRAKYOFA, METAZOA; CHORDATA; VERTEBRATA; CHONDRICHTHYES;
ELASMOBRANCHII; CARCHARHINIFORMES; SCYLIORHINIDAE; SCYLIORHINUS.
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                                                                                                                                                                                                                                   Length 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 104; DB 1; Leng
                                                                                                                                                                                              GLUCAGON-LIKE PEPTIDE.
                                                                                                                                                                                                                            Score 106; DB 1; Ler
Pred. No. 2.26e-05;
                                                                                                                                                                                                                                                                                                                                                          01-WAR-1989 (REL. 10, CREATED)
01-WAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-JAN-1990 (REL. 13, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00260; GLUCAGON; 1.
PFAM; PF00123; hormone2; 1.
HSSP; P01274; 1GCN.
SQLOGACO FAMILY; HORMONE.
SEQUENCE 29 AA; 3529 MW; 8CFE41FB CRC32;
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Gaps

1;

Indels

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Best Local Similarity 53.3%; Pred. No. 5.13e-05;
Matches 16; Conservative 6; Mismatches 7;
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50 GF
81 GI
128 GI
178 GI
20906 MW;
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MGD; MGI:95674; GCG.
PROSITE; PS00260; GLUCAGON; 4.
PFAM; PF00123; hormone2; 3.
HSSP; P01274; 1GCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 53.3%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-PANCREATIC ISLETS;
                                                                                                                                                                                    STANDARD;
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53
92 1
146 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 95247722.
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P01275;
                                                                                                                                                               LT 12
GLUC_MOUSE
P55095;
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PEPTIDE
PEPTIDE
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-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIFIDS, AND RAISES THE BLOOD SUGAR LEVEL.

-!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

-!- X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BUHL T., THIM L., KOFOD H., ORSKOV C., HARLING H., HOLST J.J.; "Naturally occurring products of proglucagon 111-160 in the porcine and human small intestine."; J. BIOL. CHEM. 263:8621-8624(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRPP (GLICENTINE RELATED POLYPEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SASAXI K., DOCKERILL S., ADAMIAK D.A., TICKLE I.J., BLUNDELL T.L., "X-ray analysis of glucagon and its relationship to receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BROMER W.M., SINN L.G., BEHRENS O.K.;
"The amino acid sequence of glucagon. V. Location of amide groups,
acid degradation studies and summary of sequential evidence.";
J. AM. CHEM. SOC. 79:2807-2810(1957).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 89327238.
ORSKOV C., BERSANI M., JOHNSEN A.H., HOEJRUP P., HOLST J.J.;
"Complete sequences of glucagon-like peptide-1 from human and pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES;
                                                                                                                                                   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACIYLA; SUIFORMES; SUINA; SUIDAB; SUS
                                                                                                                                                                                                                              MEDLINE; 81248172.
THIM L., MOODY A.J.;
"The primary structure of porcine glicentin (proglucagon).";
REGUL. PEPT. 2:139-150(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 158;
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GLUCAĞON-LIKE PEPTIDE 1.
GLUCAĞON-LIKE PEPTIDE 2.
                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 82221776.
THIM L., MODIX A.J.;
"The amino acid sequence of porcine glicentin.";
PEPTIDES 2 SUPPL. 2:37-39(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18212 MW; 9FBC1BFE CRC32;
                               21-JUL-1986 (REL. 01, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.0%; Score 104;
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PS00260; GLUCAGON; 3.
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MEDLINE; 88243712.
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56
158 AA;
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PDB; 1GCN; 30-SEP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 33-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MCDONALD J.K., MACKIN R.B., NOE B.D.;
**Processing of mouse proglucagon by recombinant prohormone convertase 1 and imunopurified prohormone convertase 2 in vitro.";
1 and imunopurified prohormone convertase 2 in vitro.";
2 BIOL. CHEM. 270:10136-10146(1995).
2 FONCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.
1- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
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GRPP (GLICENTINE RELATED POLYPEPTIDE).
GLUCAGON.
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RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
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Pred. No. 5.13e-05;
6; Mismatches 7; Indels
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GLUCAGON-LIKE PEPTIDE 2.
0B21B7BA CRC32;
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13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR.
                                                                                                                                                                                                                            01-00T-1996 (REL. 34, CREATED)
01-00T-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GLUCAGON PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 98334683.
STURN N.S., LIN Y., BURLEY S.K., KRSTENANSKY J.L., AHN J.M.,
AZIZEH B.Y., TRIVEDI D., HRUBY V.J.;
"Structure-function studies on positions 17, 18, and 21 replacement
analogues of glucagon: the importance of charged residues and salt
bridges in glucagon biological activity.";
J. MED. CHEM. 41:2693-2700(1998).
-!- FUNCTION: PROMOTES HYRROLYSIS OF GIXCOGEN AND LIPIDS, AND RAISES
THE BLOOD SUGAR LEVEL.
                                                                                                                                                                                                                                                                                                                                                                 BELL G.I., SANCHEZ-PESCADOR R., LAYBOURN P.J., NAJARIAN R.C.; "Exon duplication and divergence in the human preproglucagon gene."; NAIURE 304:368-371(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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ORSKOV C., BERSANI M., JOHNSEN A.H., HOEJRUP P., HOLST J.J.;
"Complete sequences of glucagon-like peptide-1 from human and plg
    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLUCAGON.
GLUCAGON-LIKE PEPTIDE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 53-81.
THOMSEN J., RRISTIANSEN K., BRUNFELDT K., SUNDBY F.;
"The amino acid sequence of human glucagon.";
FEBS LETT. 21:315-319(1972).
                                                                                                                       "Glucagon gene expression in vertebrate brain.";
J. BIOL. CHEM. 263:13475-13478(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 53-81.
                                                                                                                                                                                                                           WHITE J.W., SAUNDERS G.F.; "Structure of the human glucagon gene."; NUCLEIC ACIDS RES. 14:4719-4730(1986).
                     PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . BIOL. CHEM. 264:12826-12829(1989)
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MEDLINE; 89327238.
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                                                                                     88330860
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CONLON J.W., HANERH H.F., SCHWARTZ T.W.;
CONLON J.W., HANERH H.F., SCHWARTZ T.W.;
Frimary structure of glucagon and a partial sequence of
oxyntomodulin (glucagon-37) from the guinea pig.";
REGUL. PEPT. 11:309-320(1985).

I FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
THE BLOOD SUGAR LEVEL.

I FUNCTION: PROMOTED IN THE A CELLS OF THE ISLETS OF LANGERHANS
IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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                                                                                                                                                         Gaps
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SEINO S., WELSH M., BELL G.I., CHAN S.J., STEINER D.F.;
Mutations in the guinea pig preproglucagon gene are restricted to specific portion of the prohormone sequence.";
FEBS LETT. 203:25-30(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRPP (GLICENTINE RELATED POLYPEPTIDE).
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SEQUENCE OF 53-81.
MEDLINE: 86165412.
HUANG C.G., ENG J., PAN Y.-C.E., HULMES J.D., XALOW R.S.;
Gulnea plg glucagon differs from other mammalian glucagons.";
DIABETES 35:508-512(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAVIA PORCELLUS (GUINEA PIG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERLA;
RODENTIA; HYSTRICOGNATHI; CAVIIDAE; CAVIA.
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GLUCAGON-37 (OXYNTOMODULIN)
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GLUCAGON-LIKE PEPTIDE 2.
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Pred. No. 5.13e-05;
                        K -> N (IN REF. 3).
DEE43985 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                          98 HAEGTF-TSDVSSYLEGQAAKEFIAWLVKG 126
                                                                                                                                                                                                                                        PIR; A24856; GCGP.
PROSITE; PSONDS60; GLUCAGON; 4.
PFAM; PF001123; hormone2; 3.
HSSP; P01274; IGCN.
146 178 G
82 82 K
180 AA; 20909 MW;
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GLUCAGON FAMILY; HORMONE;
SIGNAL 1 20
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PROSITE: ES00260; GLUCAGON: 4.
PRASITE: PS00123; hormone2; 3.
GLUCAGON FAMILY; HORMONE; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE; 91155952.

NISHI M., STEINER D.F.;

Cloning of complementary DNAs encoding islet amyloid polypeptide,

Cloning of complementary DNAs encoding islet amyloid polypeptide,

Insulin, and glucagon precursors from a New World rodert, the degu,

Octodon degus.";

MOL. ENDOCRINOL. 1192-1198(1990).

THE BLOOD SUGAR LEYEL.

-I FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES

INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS

IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

-I SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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GLUCAGON-LIKE PEPTIDE 1.
GLUCAGON-LIKE PEPTIDE 2.
GLUCAGON-LIKE PEPTIDE 2.
AMIDATION (G-128 PROVIDE AMIDE GROUP).
; 4AIF5CE3 CRC32;
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                                     Gaps
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EUKRRYOTA, METAZOA, CHORDATA, VERTEBRATA, MAMMALIA, EUTHERIA,
RODENTIA, HYSTRICOGNATHI, OCTODONTIDAE; OCTODON.
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Pred. No. 5.13e-05;
6; Mismatches 7; Indels
Pred. No. 5.13e-05;
6; Mismatches 7; Indels
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01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                  180 AA.
                                                                                           98 HABGTF-TSDVSSYLEGQAAKEFIAWLVKG 126 |:|||| ||-|| :| :| :| || || :| :| 1 || :| :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 || :| 1 |
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Mon Oct 4 15:31:19 1999; MasPar time 10.21 Seconds 213.830 Million cell updates/sec MPsrch_pp

>MOHAM-312-CLAIM83B.PBP (1-40) from moham312177.pep 281 1 hgegtfitsdlskgmeeeavrlflewlknggpssgappps 40 abular output not generated. Description: Perfect Score: Run on:

Sequence:

179066 seqs, 54579741 residues Searched:

PAM 150 Gap 11

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_organelle
5:sp_lnvertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_blant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus Mean 34.596; Variance 60.715; scale 0.570 Statistics:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	1.79e-12	1.64e-11	1.86e-05	1.86e-05	1.86e-05	1.86e-05	1.86e-05	2.02e-04	2.06e-03	2.06e-03	4.41e-03	1.97e-02	1.22e-01	1.22e-01	5.02e-01	5.02e-01	1.00e+00	1 980+00		~ (2.78e+00
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FILAMENT-A PRECURSOR.	HYPOTHETICAL 95.1 KD P	115.	300AA LONG HYPOTHETICA	INTEGRASE/RECOMBINASE.	HYDOTHETICAL 77.8 KD P	NITELE REDUCTASE (EC		YFMJ PROTEIN.	PHAT	PEPTIDYLARGININE DEIMI	PEPTIDYLARGININE DEIMI	HYPOTHETICAL 18.1 KD P	ROSHS.4 PROTEIN.	HYPOTHETICAL 25.8 KD P	C33E10.8 PROTEIN.	PUTATIVE VIRAL TEGUMEN	CARBOXYPEPTIDASE.	ZK550.4 PROTEIN.	WINGED HELIX PROTEIN C	MEDIUM-CHAIN ACYL-COA	NEUROFASCIN PRECURSOR.	1352AA LONG HYPOTHETIC	NEUROFASCIN PRECURSOR.	VOLTAGE-GATED CALCIUM
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ALIGNMENTS

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PRT: 266 AA. 942143 PRELIMINARY; PRT: 266 AA. 402143 PRELIMINARY; PRT: 266 AA. 942143 PREMBLREL. 05, CREATED) 91-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) 91-JAN-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE) PROGLUCAGON I. XENOPUS LAEVI . XENOPUS LAEVI . XENOPUS LAEVI . XENOPUS . XENOPUS . MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.	<pre>IEN Y., BRUBAKER P.L., PEDERSON R.A., encodes novel GLP-1-like peptides wi 94:7915-7920(1997). E5139A25 CRC32;</pre>	DB 13; Length 266; 79e-12; cches 5; Indels 1; 128 33	042144 PRELIMINARY; PRT; 219 AA. 04214499 (TREMBIREL. 05, CREATED) 01-JAN-1998 (TREMBIREL. 05, LAST SEQUENCE UPDATE) 01-JAN-1998 (TREMBIREL. 06, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBIREL. 08, LAST ANNOTATION UPDATE) PROGLUCAGON II. RENOUS LAEVIS (AFRICAN CLAWED FROG). EURARYOTA; WETAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS. [1] [1] [1]
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1	araJah b ucagon (perties SCI. U.3 305016; GLUCAGO	tch al Similarity 60.6%; Pred. No. 3 20; Conservative 7; Mismat HAEGTF-TSDVTQQLDEKAAKEFIDWLINGFS : : : :	042144 PRELIMINARY; PRT; 042144.1998 (TREMBLREL. 05, CREATED) 01-JAN-1998 (TREMBLREL. 05, LAST SEQU 01.NOV-1998 (TREMBLREL. 08, LAST SEQU 01.NOV-1998 (TREMBLREL. 08, LAST ANNO NENGLUGAGON II. KENOPUS LAEVIS (AFRICAN CLAWED FROG). EUKARYOTA; MITAZOA; CHORDATA; VERTERR MESOBATRACHIA; PIPOIDEA; FIPIDAE; XEN SEQUENCE FROM N.A.
LT 1 042143 042143; 042143; 01-JaN-1998 01-JaN-1998 01-NOV-1998 PROGLUCAGON XENOPUS LAEV EUKARYOTA; P MESOBATRACH1	LINIO NA. MEDLINE; 97369292. IRMIN D.M., SATKUN WHEBELER M.B.; "The Xenopus proglinguloricopic proproctopic programment. Natl. ACAD. EMBL; AF004432; G2 PROSTER; P800260; PROMITS; P800260; PROMITS; P800260;	Query Match Best Local Simil Matches 20; Db 97 HAEGIF: 2y 1 hgegtfil	042144, PRELIM 042144, 042144, 01-214-1998 (TREMB 01-JAN-1998 (TREMB 01-NOV-1998 (TREMB PROGLUCAGON II. XENOPUS LAEVIS (AF EUKARYOTA, METAZOA MESOBATRACHIA; PIPP [1] SEQUENCE FROM N.A.
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Q1-NOY-1996 (TREMBLEREL. 01, CREATED)
O1-NOY-1996 (TREMBLEREL. 04, LAST SEQUENCE UPDATE)
O1-NOY-1996 (TREMBLEREL. 08, LAST ANNOTATION UPDATE)
O1-NOY-1996 (TREMBLEREL. 08, LAST ANNOTATION UPDATE)
PROGLUCAGON (FRAGMENT).
ONCORPHYCHOS TSCHAMTTSCHA (CHINOOK SALMON) (KING SALMON).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
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ONCORPYNCHUS MYKISS (RAINBOW TROUT) (SALMO GAIRDNERI).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; BUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
ONCORHYNCHUS.
                                                                                                                                                             "The Xenopus proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties."; PROC. NATL. ACAD. SCI. U.S.A. 94:7915-7920(1997).
EMBL; AF004433; G2305018; -. PROSITE; PS00250; GLUCAGON; 3.
PROSITE; PS00123; hormone2; 4.
SEQUENCE 219 AA; 25271 MW; 45C42A88 CRC32;
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IRWIN D.M., WONG J., WORG J., THE MEDLINE SPECIAL WOOD THE WOOLD THE MODEL TH
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"Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
MOL. ENDOCRINOL. 9:267-277(1995).
EMBL: U19913; G736361; -..
PEMBL: DF00123; hormone2; 2.
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MEDLINE; 97368292.
IRWIN D.M., SATKUNARAJAH M., WEN Y., BRUBAKER P.L., PEDERSON R.A.,
WHEELER M.B.;
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 HAEGTF-TSDVTQHLDEKAAKEFIDWLINGGPT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|||| |||::::| | : ||:|| ||||:
| hgegtfitsdlskqmeeeavrlfiewlknggps 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 HADGIY-ISDVSTYLODQAAKDFVSWLKSG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | helitsdlskqmeeeavrlfiewlkng 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 AA; 7680 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Sust Local Similarity 54.5%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=PANCREAS;
MEDLINE; 95295739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q91188
Q91188;
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01-NOY-1996 (TREMBLEEL. 01, CREATED)
01-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOY-1998 (TREMBLREL.)
PROGLUCAGON (FRAGMENT).
0NCORPINCHOS WIXISS (FAINBOW TROUT) (SALMO GAIRDNERI).
EUKARYCHA; METAZOA; CHORDARA; VERTEBRATA; ACTINOPTERXGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ONCORHINCHUS MYKISS (RAINBOW TROUT) (SALMO GAIRDNERI).
BUKARYOTA: METAZOA; CHORDATA; VERIEBRATA; ACTINOPIERYGII; NEOPIERYGII;
TELEOSIEI; EUTELEOSTEI; PROTACANTHOPIERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 95295739.
IRWIN D.M., WONG J.;
IRWIN D.M., WONG J.;
IRWIN D.M., WONG J.;
IRRING Chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
MOL. ENDOCRINOL. 9:267-277(1995).
ENBA; S78473; G999383; -.
ENBA; PF00123; hormone2; 2.
NON_TER 1 1
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TISSUE-INTESTINE, DISTAL PORTION;
MEDLINE; 95295739.
MEDLINE; 95295739.
"Trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";
MOL. BNDOCRINOL. 9:267-277(1995).
BMBL; 578475; 6999385; --
PROSITE; PS00260; GLUCAGON; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                        Score 109; DB 13; Length 72
Pred: No. 1.86e-05;
11; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          091971;
0-1007-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 109; DB 13; Li
Pred. No. 1.86e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 109; DB 13;
Pred. No. 1.86e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM, PF00123; hormone2; 3.
SEQUENCE 178 AA; 20034 MW; 2056F963 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF7AF3EC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 AA
                                                                                                                                                                                                                                                                     72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                 HADGIY-ISDVSTYLQDQAAKDFVSWLKSG 67
                                                                                                                                                         39 HADGIY-TSDVSTYLQDQAAKDFVSWLKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.8%;
llarity 43.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.8%;
                                        38.8%;
larity 43.3%;
Conservative
8293 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                        PRELIMINARY;
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hes 13; Conser
                                                          Best Local Similarity
Matches 13; Conser
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Matches

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RAPE SOC SOE PER PROPERTY NAMED IN THE PROPE

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RABIES VIRUS.
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES; RHABDOVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAURIA; SQUAMATA;
SCLEROGLOSSA; ANGUIMORPHA; HELODERMATIDAE; HELODERMA.
                                                                                                                                                                                                                                                                                                    HELODERMA SUSPECTUM (GILA MONSTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAUKIA; SQUAMATA;
SCLEROGLOSSA; ANGUIMORPHA; HELODERMATIDAE; HELODERWA.
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Pred. No. 2.06e-03;
7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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05.294
05.7294
05.7294
01.JUN-1998 (TREMBLREL. 06, CREATED)
01.JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01.JUN-1999 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01.JUN-1999 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
L PROTEIN, RNA DEPENDENT RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 97; DB 13; Le
Pred. No. 2.06e-03;
7; Mismatches 8;
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CHEN Y.E., DRUCKER D.J.;
J. BIOL. CHEM. 0:0-0(0).
EMBL; 77611; G191603; -.
PROSITE; PS00260; GLUCAGON; 1.
PROMITE; PS00123; hormone2; 2.
SEQUENCE 149 AA; 17224 WW; F763AB51 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23553 MW; EE50250D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 HADGRY-TSDISSYLEGQAAKEFIAWLVNG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 HADGRY-TSDISSYLEGQAAKEFIAWLVNG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HELODERMA SUSPECTUM (GILA MONSTER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
CHEN Y.E., DRUCKER D.J.;
J. BIOL. CHEM. 0:0-0(0).
EMBL: U77612; G1916065; -.
PROSITE; PS00260; GLUCAGON; 2.
                                                                                                                  04,
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08,
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Best Local Similarity 46,7%;
Matches 14; Conservative
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Best Local Similarity 46.7%;
Matches 14; Conservative
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012956 PRELIMINARY;
012956;
01-JUL-1997 (TREMBLREL. 0
01-JUL-1997 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                       PRELIMINARY;
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NCE 204 AA; 2355
                                                                                                                                                      (TREMBLREL.
                                                                                                                  (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
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STRAIN-RC-HL;
RESULT 9
1D 012955
AC 012955;
DT 01-JUL-1997 (
DT 01-NUL-1997 (
DT 01-NUL-1998 (
DE PROGLUCAGON.
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ONCORHYNCHUS MYKISS (RAINBOW TROUT) (SALMO GAIRDNERI).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-INTESTINE.

MEDLINE: 95295739.
IRWIND D.M., WONG J.,
RONG J.,
ROLL WOOR J.,
ROLL WONG J.,
ROLL WONG J.,
ROLL WOOR J.,
ROLL WONG J.,
ROLL WONG J.,
ROLL WOOL J.,
ROLL J.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRWIN D.M., WONG J.;
Trout and chicken proglucagon: alternative splicing generates mRNA
transcripts encoding glucagon-like peptide 2.";
MOL. ENDOCRINOL. 9:267-277(1995).
               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROGLUCAGON.
GALLUCAGON.
GALLUG (CHICKEN).
BUKARYOTA: METAGOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEGGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 103; DB 13; Length 200
Pred. No. 2.02e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
           Indels
                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 109; DB 13; I. Pred. No. 1.86e-05; 11; Mismatches 5;
       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                            178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 HAEGTY-TSDITSYLEGQAAKEFIAWLVNG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 HADGIY-ISDVSTYLQDQAAKDFVSWLKSG 118
                                                                                  90 HADGIY-ISDVSTYLQDQAAKDFVSWLKSG 118
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                                                                                                                                                                                                                                                                                                            PRT;
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01,
08,
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15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.8%;
Local Similarity 43.3%;
nes 13; Conservative
           Conservative
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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MEDLINE; 95295739.
                                                                                                                                                                                                                                                                    RESULT 7
ID Q91189 PRE
AC Q91189; Q92168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLUCAGON II.
       13;
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Q91410
Q91410;
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SEPT PROS

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Gaps

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Matches

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Gaps

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NATÜRE 368:32-38(1994).
EMBL; 270311; E1349578; -.
SEQUENCE 502 AA; 56937 MW; 82D77FDD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63300 MW; 35D63A16 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX
                                                                                                                                                                                                                                                       406 GENAKMISKMMNEKPEQSERLFVDWVEYAAKNPG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 AA
                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 DISKRIDDE-VR-YVDWLRN 500
                                                                                                                                                                                                                                                                                                                                                                               01,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIROLOGY 206:611-625(1995).
EMBL; X80191; G517241; -.
SEQUENCE 552 AA; 63300 M
                                                                                                                                                                                          Query Match
Best Local Similarity 26.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.6%;
Similarity 45.0%;
9; Conservative
                                                                                                                                                                                                                           9; Conservative
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10 dlskqmeeeavrlfiewlkn
                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JT 15
067000 PRELIMINARY;
067000;
01-AUG-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NATURE 392:353-358(1998)
                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
REPLICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 95133199,
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SEQUENCE FROM N.A.
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Q38064
Q38064;
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MEDLINE: 9415018.
WILSON R., ANSCOGGH R., ANDERSON K., BAYNES C., BERKS M.,
WILSON R., BUSTOND J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-F199;
ROMINE M.F., STILLWELL L.C., WONG K.-K., THURSTON S.J., SISK E.C., SENENCE C.W., GASTERLAND T., SAFFER J.D., FREDRICKSON J.K.;
SENESR C.W., GASTERLAND T., SAFFER J.D., FREDRICKSON J.K.;
"Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromaticivorans strain F199,",
STRMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AROTHEITCAL PROTEIN, PLASMID.
SEQUENCE 379 AA; 42269 MW; ED0127FC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
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                                                                                                                                                            Length 2127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 32.4%; Score 91; DB 2; Length 379; Best Local Similarity 37.9%; Pred. No. 1.97e-02; Matches 11; Conservative 9; Mismatches 8; Indels
                                                                                                                                                Score 95; DB 14; Length 212
Pred. No. 4.41e-03;
6; Mismatches 5; Indels
                                                                            SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL. ABOO9663: D1024994; -
EMBL: ABOO96612: D1024989; -
SEQUENCE 2127 AA; 242427 MW; 847321FB CRC32;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                           08, CREATED)
08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                379 A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 SREMAAEMAR-FLEWFAATGPGGATPLPG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 skqmeeeavrlfiewlknggpssgappps 40
                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                           10 dlskgmeeeavrlfiewlkng 30
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                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL 42.3 KD PROTEIN. SPHINGOMONAS AROMATICIVORANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01,
                                                                                                                                                          Query Match 33.8%;
Best Local Similarity 47.6%;
                                                                                                                                                                                                                   37 NLNSPLIEDPVRLMLEWLKTG
                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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01-NOV-1998 (TREMBLREL.
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01-NOV-1996 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                             (TREMBLREL.
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                                SEQUENCE FROM N.A.
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                                                             MINAMOTO N.;
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01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                        PLASMID PNL1
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RESULT OCCUPANTO OCCUPANT

LT 12 085863 085863;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAIREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCI C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN SMALDON N., SMITH A., SONHRAMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WAIERSTON R.,
WAISON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
elegans.";
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MEDLIKE; 98196666.

DECKERT-G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
BECKERT-G., WARREN P.V., SHEAD M.A., KELLER M., AUJAX M., HUBER R.,
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
acolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; LEVIVIRIDAE;
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Pred. No. 1.22e-01;
9; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 86; DB 5; Length 502;
Pred. No. 1.22e-01;
15; Mismatches 10; Indels
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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01-AdG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
APOLIPOPROTEIN N-ACYLTRANSFERASE.
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RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
RA GRAHAM D.E., OVERBEER R., SNEAD M.A., KELLER M., AUJAI M., HUBER R.,
RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL. AE0007709, G2983374, ...
KW TRANSFERASE; ACYLTRANSFERASE; LIPOPROTEIN.
SQ SEQUENCE 439 AA; 50757 MW; 7963CD20 CRC32,
Query Match

29.2%; Score 82; DB 2; Length 439;
Best Local Similarity 35.1%; Pred. No. 5.02e-01;
Matches 13; Conservative 10; Mismatches 13; Indels 1; Gaps 1;
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Search completed: Mon Oct 4 15:31:31 1999 Job time : 12 secs.

384 SEGTFQHMKLARVRAIENEKFEL-WVNNTGPSGIISP 419 :|||| || ::| |||| :| || || :| 2 gegtfitsdlskqmeeeavrlfiewlknggpssgapp 38

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